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(54) Title: BIALLELIC MARKERS

(57) Abstract

The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(AA) = x^2$
 Homozygote: $p(BB) = y^2 = (1-x)^2$
 Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
 Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

- 15 The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

- 20 These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25
$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + y^4 + z^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

- 30 The cumulative probability of identity ($\text{cum } p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

$$\text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing
30 the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined a priori, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACCTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGCTCT
						GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAGAGAGAGAGTTGAGACCAATCTTTATTT
						GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAAAGCTTTTGGAGATAATGT
WI-7070	226	CT	---		---	TACTAGACTTTATGCCATGGTGCTTTCTAGTTTAATGCTGTGCTCTGTCTGTCAG
						AAGCCATTGACGTAACTCTCAGAGGTTATTGCGATGGATTGACTCTGGGACAAAAGGAC[G/C]AA
						AAACACTCTTCTGTGGATATCTGTGCAGATAGATGCCCAAGATCAGATGCTACCCAGATGTGTTTT
						GATAATACATAAGCCCTAGGATTAGATACAATCTTGAAAGAACTGAGACAGATAATTCTGAATT
WI-10744	61	GC	---		---	AAATGAGGTAAAGTTTCAGGCACCTCA
						GGGCAATTACCAGCAAAAAGTCAAAATTACCAGCATCAAAAGTCAGGTGCAAGGAGGTAGAACAA
						TTACAGTAAGTGTCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCCTAGAAATA[C/T]AGTG
						GGTCCCTAATAGTTATTAGTCCCTTTTCTCCCTCTTCTCAATCTCTGAATTTATTTTATACTTAA
WI-9975	126	CT	---		---	GGGATTAGTTACCACCAAAATGTGTATGTATCAATTTGATTTACTGAA
						GCTAGGTTTGTCTGTGGCTGCTTCACTAGACTTGAGATGACTTGATTACAGTATCCCTATGT
						GATGTAAGTGTAGACCTTCCCTTCTCCGCAATCCAGCTCCAGTTTCAGAAAAGTATGCCACAC
						TCAACCTTCTCTCCAGTTCATCCTGTATTAAATTTCTCCCATATTAAATCAAGGGAGTGGACAGGT
WI-8010	247	GT	---		---	CCCTGGCTGAAAAGAAATAAAGATCCCCAAAGTGGTGGG[G/T]CTT
						GCCGGCCTATCTTTTAAATTTAACTTGATCTTTGGTGTCTTCCATCTCCTAGGATTCGCTTATAAT
						CTTTGTCTGTCTGT[G/C]ATTACCTGATCTACTTTTGTACACAAGGCTGATGGCTCACAATGT
						AGTAGTGCCAAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	GC	---		---	TCTCGACTCTATAACAACACTCCAACAGAA
						GCCGGCCTATCTTTTAAATTTAACTTGATCTTTGGTGTCTTCCATCTA[G/C]GATTCTGCCTTAT
						AATCTTTGTCTGTCTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGTGCCAAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	GC	---		---	TCTCGACTCTATAACAACACTCCAACAGAA
						TATGCACCTTCCACAAAAGCGATATAATTTAAAAGTTTTTTCATTAGAAATAATGTATAAAAATAA
						ATATGTTATTATAGGCATTTTACTAAGTATAGTCTCTTGGAAAGGAACACCCCAACCAATACTT
						ATAAAGTACATGTAAATTTATAGTAACATATTTACTATATACATATGGAATAATCATATTCTCACA
WI-8007	242	CA	---		---	GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAC[G/A]AGCTGCTG
						TCAGTTGCAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGATGTTTGTAG
						TCTATATTCACACATATGAGTGAATTTCTGTTGGGCGATGGGAAATACATCTTTATGAGACATTGA
						ACTGCTCACCACATCATAGTATCCATTTAAACAGACCAACAAATGTATAGAATTCCTTTGTTTAC
WI-9823	97	CT	---		---	ATGCTTCCAACTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	TCTACATTCTATGGACAAACCTCCATGCCCTTTCACATGCTGATCCCTCCTCCTGGAATTCCTTCCT ACTTGCTCATGTACAATTTCTGCTGCTCTTCA/TJGGGCGAGCTTGAAGCCTCCCTTTAGAC ACCTACAGGTACAGCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCCTCTG TCTTTAAACCTGTAAATGGTATATTATCCTTGGGTGTTGAATGTCCTC
WI-9651	139 T C ---	---	TCTACATTCTATGGACAAACCTCCATGCCCTTTCACATGCTGATCCCTCCTCCTGGAATTCCTTCCT ACTTGCTCATGTACAATTTCTGCTGCTCTTCAAGGGCAGCTTGAAGCCTCCCTTTAGACACCT CT/CACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCCTCTGT CTTTAAACCTGTAAATGGTATATTATCCTTGGGTGTTGAATGTCCTC
WI-7676b	309 A C ---	---	GTGACCTTCTGCAGCGTGGAGATGGACATCCTTGTCTGCTGGGACCTTGGCCCTGCTATTATTTTG TATTTATGTCCTTAATCTCTTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTCTCTTGGTGGCTGCTGGTGGTGGAGGGGAGGAGCGTGTGGACTGCAGCTTCTGCTGTGC TCCCCCGTCTCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCTGCAGCGTGGAGATGGACATCCTTGTCTGCTGGGACCTTGGCCCTGCTATTATTTTG TATTTATGTCCTTAATCTCTTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GC/TJGGCTCTCTTGGTGGCTGCTGGTGGTGGAGGGGAGGAGCGTGTGGACTGCAGCTTCTGCTGTG GTGCTCCCCCGTCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGCTTGGTCTGTTCACTTCTCTCTCCTCAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGAGTTTGAATATTTTGTG/TJGACTCTATGCATGATAAATTTGTTA TGCTGTCTCTTATCTTCTTTGTTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAGGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAATATCTTTT
WI-9986	42 T C ---	---	TTGGTGTGAACCTCAGAAATAGGGAAAATAAGACAATTTGA/T/A,CJGTACCCCGAGGAACAAGAG CCCTGCACCTTGACTCCAAAAGGAGTTCTATTATCTGGCTGTTCCAGACTTATTGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAAT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGCCCTGCACATGCAAAACCTCCAGTCCCTGCTTCAAGAGCTGAAAAGGGTCCCTCGGTCTTTTATTT CAGGGCTTTGCATGGCTCTATTCCCTCTGCTCTC/AJCCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGAACAAGCTCATTGTACAGTGTCTGTTCATGAATAA
WI-7224	134 T C ---	---	ATAAACCTTGTGTATGATCACCACACTCAATAATTATCACTTATGTGCTATCAGATATCCTCTCT ACCTCAGCTTATTTGAAGAAAATCCTAAACATCAATCTTTCATCCATAAAAATGTCAGCATTT /CJATTAATAAACATAACTTTTAAAGAAAACATAAGGACACATTTTCAAAATTAATAAAAAATAAG GCATTTTAAGGATGGCTGTGATTATCTTGGGAAGCAGAGTATCATGCTAG

WI-10826	132 A C ---	---	TCTATTTCATTTACAGTAGCCCATGAAGTAGGTAAACAGCCTCTATTTAACATGAGAAGATGGAGCCTTTTCCAAATGGACTAAGTAATGTGCTCAGGTTTTCTTAATAAGCAAGACCTGCA/CJCCCTGGCTCTCAGTCCAAAGCTTATCCCTTCATGCTGTTGCTGTCAGCCAGGACCCCATGCGCA
TIGR-A004S25	145 G A ---	---	GAAAGCCAGCCTCTCCATCCCCACAGATCTGCCATTAGTATTATTCCTTTGAAGATACTTTGGAGATTCAATTTCTTGAGTGGCACTGCATGCTCATTCAAGTGAACCTTTGGGGTATAGAAATGGAATGGAGAGTTTCAACAGCTTTGCTGAAACGTACTTTGGG/GA/CTCCAGACTTCACTGTCCTTAGGCATTGAACCATCACCTGGTTTGCACTTCTC
WI-1021	24 A T ---	---	ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAACAAACACAGAAATCATCAAGGAC/A/TATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATGTAAGAAGTAACCTGAAATAGTAGGATAGTATTATCATTTCTGTGTAAATAGATTCACCTCTCAGCAATGGTCTGTTTTCATTTCTATGGAACCTCTCCGTAAGTAAATTTTCAATTTCTATGGAACCTCCCCATACTGTAAATGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATGAACACACTTTTGAATGGTCTTGTCCTTCAATAAAAGAGTGACATGATTGAACATGTGTTTAGATAAGGGCAGCTT/GTJGACGGAGTGTTAGGATGAAGAGAGAGAGATTAAAGGAATCAGGAAGAAAGTAGCAATGGGAATGAAATAAGGAGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107 T G ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTCTTTGGGGTGTGAGCGGATTATGCTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCTCTGTGAGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAGTGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTCTTTGGGGTGTGAGCGGATTATG/AJCTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCTCTGTGAGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAGTGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	TCAACAGCCTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTTTACCTGTAGGAATACTGAGCTCCGATGCAGGGGAATGGGGTGGGGGTACCACCTTCTCTGACACTGCCAAGTTAAAGAAACCCCTGCTTCTGGAGAGGGAGGGCCAGACAGGAGGAAATCAAGGGCATGTATGGCTCAGTCCCACTTCTG/CJACTGCAGAGTATAGGACCGGGTTCCAACTTT
WI-9484	178 G A ---	---	TCAACAGCCTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTTTACCTGTAGGAATACTGAGCTCCGATGCAGGGGAATGGGGTGGGGGTACCACCTTCTCTGACACTGCCAAGTTAAAGAAACCCCTGCTTCTGTGAGAGGGAGGGCCAGACAGG/GA/JAGGAATTCAGGGCATGTATGTGCTCAGTCCCACTTCTGACTGCAGAGTATAGGACCGGGTTCCAACTTT

WI-7330	207	C T	---	---	AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAATTTGGGCATATAGGTTT GTGACACAGAAGTCTACTTTGGTGGCTAAAGTTTACTAAGGAAATAAATCTGAAAGATTAAG TGAGAGCTTTGAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTACAG
WI-9443	211	G A	---	---	TTAAACACAGTTTCAGGTTGGTGAAGCAGAAAGGATGTGATTACAATTTAAATGAATCAGTCACCT GCACAAATTAATCTCTTGGCATCATACAAACTGGGTTTAAATGGCAAATGATGACATCATAGCATGA CCAACTCATGGAAGGCAGTCTAGAGTCCATCAGCTCAGCTGAGGGGAAAGGCACTGCACCCA CTGACGAGACGACAGAGACCTTGGACTACAGATGACACACACATGCCACCTT
WI-7166	59	C T	---	---	TCTCTCAAAAGAGAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTAICTTGGAT CATCAACAAGATTTCTTGTGCAAAATATTTGACTATTCTGTATCTTTCATCTTCTGACTAAATTCGTG ATTTCAAGCAGCATCTTCTGGTTTAAACTTGTGCTGTGAACAAATGTGAAAGAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189	T C	---	---	GCTTCTCCCCAGGAAGCGGGTCTTGGCTGTGAACCTTCCAGAGAGGGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGCGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAGTTCJTTGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGCTC
WI-7259	188	G T	---	---	GCTTCTTCCCAGGAAGCGGGTCTTGGCTGTGAACCTTCCAGAGAGGGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGCGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAGTTCJTTGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGC
WI-7322	275	A G	---	---	GTACTTTAGGCTGTGGAGGTGGCAATTTAGTGTGACCTTGCCAGGGTTTCTAACAGATGAC CCTGTGAATCATAAATTAACCTGCATATATTTATAGCCAGTCAATTTGCCCTCTCACCCCTATATG GCCATAAAGTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTC TGGTCTCTATCCCCTTGTACATAGAGAGTTTGTATGGGGCCCAACTTCCCTGGCTG
WI-7685	46	T C	---	---	TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTGGGCTCTTCJTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAAGTCTTGGAGCTGAGCCCTCTCACCTGTACTCTTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCATGGCTTCTCTCCCTCTGCGGACTC CTGGGTTGAGCTGTGCTCAGTCCCCCAACAGATGCTTTCTGTCTC
WI-563	87	G A	---	---	TGTGACCAATTTATTTAGAGGTTTAAACATGGCTGACTATCACCTGATGGTGGCCAGAAATTC CTGGGGAGGGCTCCCTGAGCCCTGATGCTACCTAACTGCTACTTAACAATACTACTCC TGTGGTATGGGATCCTAAGCCAAAAGCTGAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191 C A ---	---			GACCAGGGCACAGAAAGCCACGGAAAGCCACAGCCACTAGCCCTGAACCTTGACACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCAACACCTTCCAGTCTTATCTGCTGTGTCAAAATGATCCTCT GTTGCTGCACCTGTCATTACTGTTGATGGATTATAATTATTGTCCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81 A G ---	---			GACCAGGGCACAGAAAGCCACGGAAAGCCACAGCCACTAGCCCTGAACCTTGACACACCCCTGGAGTT TCTCTCCCTCCCT[A/G]TCCCTCACCAACACCTTCCAGTCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACCTGTCATTACTGTTGATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31 A G ---	---			GACCAGGGCACAGAAAGCCACGGAAAGCCAC[A/G]GCCACTAGCCCTGAACCTTGACACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCAACACCTTCCAGTCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACCTGTCATTACTGTTGATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91 C T ---	---			GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACAACACCCCTGGAGTGGGATGGCAGA GACATCCACCTTAGCAAGTGGG[C/T]ACCTACTAGAGCAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGACG CTGAGCCACTCTTAAACCATGAACCATCAACATTTAAATAACGTTGCCCCCCC
WI-10870	103 G A ---	---			GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACAACACCCCTGGAGTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGACCTACTTAGA[G/A]CAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGACG CTGAGCCACTCTTAAACCATGAACCATCAACATTTAAATAACGTTGCCCCCCC
WI-7719b	281 T C ---	---			AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCCTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTCTGGACATTGCCCATGTATATCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163 A G ---	---			AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCCTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATATCTCACTGATGATTTCAAGCTAAA
WI-10396	72 C A ---	---			GCCTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]GTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTGA TGCCATTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTGAGG TTAACAGCCACATTGTAAACACTTTGT

WI-10673	94 C G ---	---	---	TCCCTTATGCACCCAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGTGGCACTCATGGAGGGGCG/GTGCAGGTGGAACATATGCACTATGCACTGCTCCGGCCACACA TCCTGCTGGGCCCCCTACCCCTGCCCAATTCAATCCTGCCAATAAATCCTGCTCTATTGTTGTCATCCTG GAGAAITGAAGGGAGGTCAGTGTGTTGTCAATGATTGTGACAGAAACCT
WI-7842	57 T C ---	---	---	CACAGCCATGCCCCTTGAGGAGCCGGCCACCAAGTGTGAATCCCCTATCCCATTGTC/GGTATGAG TCCCAITTTGCCTTGCAATTAGCAATCTGTCTCCCCCAAAAAGAAATGTGCTATGAAGCTTTCTTTCT ACACACTGTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTACAGCTCCCTTATA
WI-7721	145 A C ---	---	---	CTGCCATCACGCCCACTGGAGTCCACACTTGAATTTGGGAGCTACCACGGGTGCCATGCTCTGG AGGACAAGGGGGCCACATCCCACCCACGCTGTACCCAGCCGGGAGGTGCAGCCCTTCTCTCC TGCTCTGCA/GTCTGACTCTCTTTGAGGTCCCTGTATGCTACCTCTGACTTCTGTGTTGTTCCCTCTG TGCTGCTCTCATCCATCCTCTTACTGGGGCTGGGGCTCTAGCCCAA
WI-4767b	173 C A ---	---	---	TTCCAGTCTGTTTATCCCTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCCT CAGGTCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACA/C/AJAAATCACTAAGGAATTCACACTAAGA CTCCTCTAACCCAGAGATTTTAAACCT
WI-4767	50 A G ---	---	---	TTCCAGTCTGTTTATCCCTTCATTGTCAAAAAGATGCTCTTAGACTGA/GA/JATTTCATAAAGAGTT CCTCAGGTCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATG TTCTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCACACTAAGAC TCCTCTAACCCAGAGATTTTAAACCT
WI-7718f	222 C T ---	---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATACAAAGAA/C/TJCATGCAGGAAGGAAACTATGTATTAAT
WI-7718e	60 T C ---	---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT/CJGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAT
WI-7718d	31 G A ---	---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAT

WI-7718c	91 C G ---			ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAACACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248 A G ---			ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAACACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAA/GJAT
WI-7718a	42 A T ---	C		ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGTC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAACACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTA
WI-7227d	99 G C ---			AGGGAATTGTGTTGCTCTCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCAATGGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---			AGGGAATTGTGTTGCTCTCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC GGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCAGAGGACTGAGCTAAACAGTG TTATTATGGGAAGGAATGGCAATGGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---			AGGGAATTGTGTTGCTCTCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCAATGGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---			AGGGAATTGTGTTGCTCTCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGC TTCCGTGGACCAATTCATCTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCAATGGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---			CCCAATGCCTCTCCAGATGTCAGGACTCTGCTGCTCTGGAGGTGGAGACAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGCTATGTTGTGATCCTTCATCGAACAACTGATCGGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCAACATGATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGCTGGAGGTGGGAGACAAGGAACCTTAA JCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCTTCATCGAACAACACTGATCGGAA AACTTGAATCTGTACTGAAATGAGGAGAGAGACATGTCTATTGAACCTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	OCAGAACACCTACACCTTGTCACCTGCCTGGGACTCCTATGATGGCTGCTGTTGATAATAATCA GATCATGCCAAGACGGCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAATCGCTCC CTGAGGAGAAATCTGGAGAGCTGAGJGTGTGATGAAGGTGATGTTGGAGGGAGCACAGTGT CTGTGGGAGCCAGGAAGCTGCTACCCCAAGATTGGTGAGGAAACTA
WI-7878a	51 C G ---	---	CCAGAACACCTACACCTTGTCACCTGCCTGGGACTCCTATGATGGCTGCTGJGTGTTGATAATAA TCAGATCATGCCAAGACGGCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAATGC GTCCCTGAGGAGAAATCTGGAGGAGCTGAGTGTGATGAAGGTGATGTTGGAGGGAGCACAGTG TCTGTGGGAGCCAGGAAGCTGCTACCCCAAGATTGGTGAGGAAACTA
WI-7381c	213 C T ---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTTCTTTCTACC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGTTTCTGCTATGTTGAGATC AGATGTGGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGACA AAACGGCTCCTGCTGCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTGCTTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGTTTCTGCTATGTTGAG ATCAGATGTGGCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTGCTTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGTTTCTGCTATGTTGAG ATCAGATGTGGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	AAATTGCTCTATTGGACCTTCATATTAATAAGAGCAATGAGAGCGGGAATAATTGAACCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GATGTAGATTGTCACATTCAATCTGAAACAACCTG CCAGGCAAGTCTTCTCCCATTTACAAATAAGGAGACAAAATTAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	AAATTGCTCTATTGGACCTTCATATTAATAAGAGCAATGAGAGCGGGAATAATTGAACCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GGATGTAGATTGTCACATTCAATCTGAAACAACCTG CCAGGCAAGTCTTCTCCCATTTACAAATAAGGAGACAAAATTAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC



WI-1795b	130 TC ---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTCTCCAGACTCCTACGATTAA AATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGCAGAAAGAAAGT/CJC GTCTACCAATTTTACCACAAATTCGTAGTACAAATTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47 TC ---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTT/CJCTCCAGACTCCTACGA TTAAATGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGCAGAAAGAAAGT/C GTCTACCAATTTTACCACAAATTCGTAGTACAAATTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136 GA ---	---	CACACAATTTGCAACACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATAGTAGGTCCTGGTCTCTCTATCACATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGCCCGCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616c	136 GA ---	---	CACACAATTTGCAACACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATAGTAGGTCCTGGTCTCTCTATCACATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGCCCGCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616b	141 CT ---	---	CACACAATTTGCAACACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATAGTAGGTCCTGGTCTCTCTATCACATTGCCA CGTAGC/CJCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGCCCGCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616a	116 GC ---	---	CACACAATTTGCAACACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATAGTAGGTCCTGGTCTCTCTATCACATTG CCAGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGCCCGCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-1126c	52 GA ---	---	CTCTTATTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTG/GAJATAATAATA AAACCCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAA AATTTATTCTCAAGATATAAAATAAATAATTTAATTCAGTTTCTCAAAAGGAATATGAAATT TGTTAAATGCAATCCAGCTGTAACCTTTTGGACTTGCTTTTATTTCT
WI-1126b	230 TC ---	---	CTCTTATTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATCACTAATAAAAA CCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAAATTT TTATTCTCAAGATATAAAATAAATAATTTAATTCAGTTTCTCAAAAGGAATATGAAATTTGTT AAATGCAATCCAGCTGTAACCTTTTTCGAGACTTGCTTTTATTTCT

WI-1126a	97 T C ---			CTCTATTCTCTGGGCACTGCTTCTTTGGGGCAAACTCCAGTATCACTGATACATAATAAAAA CCCTGTAAAGTCTGCTTGCAATTTCAAGATT/CJCAATATATATCCAGATTGTTTCCAGCAAGAAAA ATTTTATTTCTCAAGATATAAAAAATAATATTAAATTCAGTTTCCCAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACTTTTGGACTTGCTTTTATTTCTT
WI-11183c	124 C T ---			TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGTATTTTGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGAGGATAGAGTTTAAAT/CJJA TTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---			TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGTATTTTGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGAGGATAGAGTTTAAAT/CJJA TTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---			TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGTATTTTGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---			GCTTGGTTTGCTTAGTCTTATTGCTCAGTCTTGAGTTCTCCCTTCTGCTGGCCCTTTTGATTTCA CCCATACCTCTATGCTCGCTCAGACCAATTCCTCTATCTGGAGCGCTCTTCCCTTGACTTTCTCTG TTCACCAACCTTCTTTTATTTCTCAGGACACTCA/GAJTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCCTCTTCC
WI-10770a	49 G T ---			GCTTGGTTTGCTTAGTCTTATTGCTCAGTCTTGAGTTCTCCCTTCTG/JCCTGGCCCTTTTGATTT TCACCCATACCTCTATGCTCGCTCAGACCAATTCCTCTATCTGGAGCGCTCTTCCCTTGACTTTCTC CTGTTCCACCAACCTTCTTTTATTTCTCAGGACACTCAGTTCCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCCTCTTCC
WI-9667b	82 C T ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGCTCATGACACTTTTCAATCTCTGCCTTGATCATGG TTATCACTGGACA/CJTAGCCACCTCCCGAGCGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT
WI-9667a	68 G C ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGCTCATGACACTTTTCAATCTCTGCCTTGATCATG G/CJTATCACTGGACACAGCCACCTCCCGAGCGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT

WI-10400d	189 A G ---			ACATTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACCTTACTAACACAATAATTTATTCTAATTT TCCTCCCTTACCTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCAGTGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---			ACATTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACCTTACTAACACAATAATTTATTCTAATTT TCCTCCCTTACCTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---			ACATTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACCTTACTAACACAATAATTTATTCTAATTT TCCTCCCTTACCTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---			ACATTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GCTGTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACCTTACTAACACAATAATTTATTCTA ATTTTCTTCCCTTACCTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---			AAAGGGCTACAAACTAAGGCCAAAACCAATGAACGGTATAAGGAGGGTAATGCAAGGGGAGACCC CACCTCTCACCACCTTTAGAAAAGGGCATTTCAGCACATTCATGAGGCTTCATATACTGGTTAG CAACAATGGAATGATTAGCCCAAGGCGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---			AAAGGGCTACAAACTAAGGCCAAAACCAATGAACCTGATAGGAGGGTAATGCAAGGGGAGAGA CCCCACCTCTCACCACCTTAGAAAAGGGCATTTCAGCACATTCATGAGGCTTCATATACTGGTTAGC AAACAATGGAATGATTAGCCCAAGGCGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATTGAT CATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGA[A/C]GACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA

WI-7038a	31 G A ---			CGAGCTTGGGATAAGCAAGGGGACCTTGGCGA/JCTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAAATACTGAGATGCTGGGCTCTCTCCCTCCAGGAATGCTGGCCCCCAGCCTGGCCA GACAAGAAGACTGTGAGGAGGGTGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCTGCAATTTATGGTGTAGTTCTGA
WI-3429b	64 G T ---			ATACGCTTCTGTCTGCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCCGAGTCCACACA(G/T) CCCTCAGCCCTTCAGCTTTCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCCTCTCTGGAATTTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTTCTAAGCAACGACGGAGC
WI-3429a	62 C T ---			ATACGCTTCTGTCTGCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCCGAGTCCACACA/C/AG CCCTCAGCCCTTCAGCTTTCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCCTCTCTGGAATTTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTTCTAAGCAACGACGGAGC
WI-6786c	151 G A ---			ATTTAGGACAGTGAATAAAGGATTTATAATAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCTAGATGAAGTGGCTTCTTTGGCGAAGGATAAAGAGTGAAGTGAAGTGAAGTGA GTGAGCCCCATTCTTGA/JTGGGATAAGGTGTCATTTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786b	111 A T ---			ATTTAGGACAGTGAATAAAGGATTTATAATAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCTAGATGAAGTGGCTTCTTTGGCGAAGGATAAAGAGTGAAGTGAAGTGAAGTGA CCTGTGAGCCCCATTCTCTGTGGGATAAGGTGTCATTTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786a	106 A T ---			ATTTAGGACAGTGAATAAAGGATTTATAATAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCTAGATGAAGTGGCTTCTTTGGCGAAGGATAAAGAGTGAAGTGAAGTGAAGTGA CCTGTGAGCCCCATTCTCTGTGGGATAAGGTGTCATTTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6711b	226 G T ---			GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTAAACCTCAGTTCCAACTCACTGAAT TTCATATACCTCCATTATTAATCAATACATCATTCAGAGAAAAGACAACGGTGCCAACTGGGTT TGTTGGTGGCTGCACACCCACAG/JTGGCAACTAAGTGTAACTCTCTAAA
WI-6711a	36 T C ---			GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTAAACCTCAGTTCCAACTCACTC GAATTCATATACCTCCATTATTAATCAATACATCATTCAGAGAAAAGACAACGGTGCCAACTG GGTTTGGTGGTGGCTGCACACCCACAGTGGCAACTAAGTGTAACTCTCTAAA

WI-10613b	172 A C ---	---	ATTTGATGCCAAATCATAATACCTGGCAATCTAGAAACATACAGTGTAAATAGAAATTTTGAGCCATA TGGTGAAAAATTTAGAAATATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTTT TTTGCAACTTTTGACAAGGCCAGGCAATTTTATTG/C/GC/CCTAGGAGGTTACTATAATTTAGA AAGGCTCTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ---	---	ATTGTATGCCAAATCATAATACCTGGCAATCTAGAAACATACAGTGTAAATAGAAATTTTGAGCC ATATGGTGAAAAATTTAGAAATATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ---	---	GCCTAGTGGGAAACCTCAGGTAGTCTCCGAAATCTGTGCTTTCCAAACAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCTCTTTTCCAGCCCTGAGGAA/A/ TJGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587b	81 G A ---	---	GCCTAGTGGGAAACCTCAGGTAGTCTCCGAAATCTGTGCTTTCCAAACAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587a	28 C T ---	---	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAATCTGTGCTTTCCAAACAGTGACTACCCCTTGA AGCATATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-10681b	103 T A ---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTAAAGAGCC/T/AAAGACAGGCAATTTTATCCTAATTCG TAGTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAGGAGGTGACGCTCTGTTAAAG
WI-10681a	41 A T ---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAGAGCC/T/AAAGACAGGCAATTTTATCCTAATTCG TAGTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAGGAGGTGACGCTCTGTTAAAG
WI-7222c	126 G T ---	---	GCCTCTCCTCAACTGTCTGGACCAAGGCTAGGAAAGGCTGTGAGATGACTGTGGTCCCTCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTCTCAAGTTGGGGATGGG/G/T/ATAA AGGAGGGGAATTCCTTGAACAAGAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAGACTCGAATTCATTT

WI-7222b	255	GA	---			<p>GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTGGTCCCCCTTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTGGGGATGGGAATAAAGG AGGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTCTCA</p>
WI-7222a	126	GT	---			<p>GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTGGTCCCCCTTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTGGGGATGGG[GT/AAATAA AGGAGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTT</p>
WI-8054d	41	CA	---			<p>AAAGATGACACTTTAGAACTGGATCACTTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT CTTGCACTCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCCTCAAGCCTTAGCAAA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTAGTTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCTGGGCGTACAGAGATCCTTGGCCCTT</p>
WI-8054c	237	GT	---			<p>AAAGATGACACTTTAGAACTGGATCACTTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCCTCAAGCCTTAGCAAA TCCTCTTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTAGTTTGCCACCATAGCCACTCTGCTTCC TGTCATAACGCCGCTTTCCTGGGCGTACAGA[GT/AAATCCTTGGCCCTT</p>
WI-8054b	148	TC	---			<p>AAAGATGACACTTTAGAACTGGATCACTTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCCTCAAGCCTTAGCAAA TCCTCTTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTAGTTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCTGGGCGTACAGAGATCCTTGGCCCTT</p>
WI-8054a	131	CG	---			<p>AAAGATGACACTTTAGAACTGGATCACTTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCCTCAAGCCTTAGCAAA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTAGTTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCTGGGCGTACAGAGATCCTTGGCCCTT</p>
WI-10854b	152	GT	---			<p>TTCCAAAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACACGAGACGATAGTTAACGCTGTGGTAAGTTTAT ACGGTGTGCGAGGCAACA[GT/GGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATTCTTGCTG TTTTAGACACAGGGTCTGCTGTGTG</p>
WI-10854a	102	CT	---			<p>TTCCAAAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACAC[GT/GAAGACGATAGTTAACGCTGTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATTCTTGCTG TTTTAGACACAGGGTCTGCTGTGTG</p>

WI-9826b	127	G A ---	---	---	AATTTATATGTGAAGGTTAGCAAACTATGCCACAGGCCCATCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTTTGCACGAGTTGAGCCATTGTGACAGAGGCTGTATG/AJGCCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125	A T ---	---	---	AATTTATATGTGAAGGTTAGCAAACTATGCCACAGGCCCATCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTTTGCACGAGTTGAGCCATTGTGACAGAGGCTGT/AJGGCCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60	T G GTGGTTTTT	TTTGTGTGT	TGACATTATAT AAACGTAAAA GAAATGT	CGGACACGTTATATACAAATACAGATCGTATGGTTTGTGTGTGGTTTTTTTTT/GJTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G A G	AACTGCAAAT AGGAAACCAG	CCACCTGGGGC TCCC	TTCAAGTAACGTCAAAATAGGAAACCAGAG/AJGGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGGAGGAGGTGGCCCTACACCCCTTAT
WI-8170b	259	G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGGTGAGAGATTACAAAGGTTAAGATCATGTGTCCATCAAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAAATGAAATCTACGGAAAAACATAACAAGA
WI-8170a	204	T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGGTGAGAGATTACAAAGGTTAAGATCATGTGTCCATCAAAAGTGCAATCCTATCAATCAGAA AT/AJAAAGGTAAAGGGCCCTCAAAATGAAATCTACGGAAAAACATAACAAC
WI-8172	136	C G G A C A	CCTTATTAAA ATTGTTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCTTAAAGTCATCTTCCAATACTCCAGGTACATGTTGAAGAGTCACTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCTTTTAAATGTTTCTTGACAT A/C/GJAGTACCTTTACAGGTATTACATTTCTCTTACCCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAAATTTCTGT	TGTTGTTGAAAT CAACCTGC	AGCAGGGTTTGAAATTGATCCCTTATTTACATGAAATAAACAATTTCTGTTCG/AJGCAGGTT TGATTTCAACACAGTTGAATCTGTAAACCAAGCTGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T ---	---	---	GCTTTATTGGGATTGCAAGCGTTTACAAGGTTAAAGACAAAACCCAGCATGGGATTTTGC CGGAAT ATTAGCGTTAAAGGAG/CJTTGAGTTGAGTCAACACACGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCAGGGAAGGTTAGTGGAG/AJGAGATGGTCAGGCTTCTCTG TTCTTTAACAGCAGAGGCCCAACCTAGAACGCCCTCACCTAGCCTCTTAAT

WI-8827	22 C T	TOOCTGGGAG TTTAGTGTTCAC	GCGATTAGGAT C	GGTGCCCTGGGAGACTATGGC/TAGTGAACACTAAATCCTAATCGCCATGCAATGGAATTATT CCGACTATTACTTTCTTAGTCCCTCTTATCCACCCAGTCTTCT
WI-8833	51 A T	TCTTCCATGGC ATTCTCTG	CCTCACACATT ATAGGGCA	CTCCGGCCTCTTAAAGCTCTCTGTAGACTGTCTCTCCATGCCATTCTCTG/A/TJGCCCTATAATGT GTGAGGTATTACAATAGTCCCTATTCAAAGTCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTtagccatgttggtAAAAGTTTCATTTTcagTACATGGGTAAACCCAGGCCCTTTCCC/A/GT TATATCCAGGTATGCTACAAGTTCTTTAACTCTATCAGAAGTTATTATTACTGTTTCTTtagAGAG GCTACCAGGCTAAATTCACCTAGTTGGTTTGTCTAATGTCCTCATTTATTCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCT	CAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT/A/GJCTGCCCTGGCTGTTTGGCTCTGGCTTGTGTTTGGTTTCTT TCTCTTCTACTGGTCTTCTTTTGCTTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCGGGCATTG AGGATA	AGTCTTCTGA GCTTCCAT	ACTTTCTTGAGCTGAGCAACCTCATCTCTTtagCTTCTGGTTGATAACGCTGGTTAATCCCGGG CATTGAGGATA/C/TATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52 A G	---	---	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCTGTCGAACA/A/GJACAACATGCT TCGGACTTACCAAAGGAGAGTGGAGCTTTCCATATAAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT CA	GGTAAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA/T/CJGGTCGAACAACAACATGCT TCGGACTTACCAAAGGAGAGTGGAGCTTTCCATATAAA
WI-8895	32 A C	---	---	GTGCCACAACCTGGACACCAACCAACAGAAAT/A/CJTCGCCGTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACAGGGATGCTCCAATCGCTCTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATTTGTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTGGATGTCACA/G/CJTTATGTCAAGTTAATAAACAATTTCTAAGTGTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTCACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTCTGGCTCAGTCAACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCAGTGCATATTCTATGGAAA ATTATATCTCAAGTAAGTACAGCTAGCCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA/A/GJTTAGTATATAGAAATAATACGCAGCTGTTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGGCAG
WI-8496	41 G A	---	---	TTTCATCATCAAAAAGTTTCTTTCCATAGAAGAAATGGTAATG/AJTTGTATCAGTGCATATTCTATGG AAAATTCATATCTCAAGTAAGTACAGCTAGCCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATAGGCAGCTGTTAGAAAAAGTCT TGTTGGCCAAAGTGGGATAAAACAGTAGCAGTGGCAG
WI-14153	28 A G	GTGCAGGAAG GOCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGOCAGC/A/GJTCCTCTGCGGTTGTCACCCACATCCACAGAGCA GCCCTAGTGCAGGTGACGACCTGCCACCCACGGGACACGGGAACAGGACCCATGCTGC

WI-12108	40 C T A T A	TGAAAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGAAAAGGGTTAAACTCAAATATC[CT]GAAATACTTTTCATTATACCAGGT CAAGAAAAATGCCAGCCAGAAAAATTTATTTTAA
WI-5989	29 G A C A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAAAACGTCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCCTAAAGAAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTTAAAAAAAAT CTTGTTAACTTGCCTCCATCTTTCTTGGGTGAGGACACC
WI-12201	61 C T C T G C A T G	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTCTCTGGAGTGTATGTCCTCCAGCCCACTGATCACCTGCGATG[CT]GCCA GGTATGGTGGGGGTGATGGACGTGGGTTTGACGCCCTCCACTGCTCGATAAAGGC
WI-12018	31 A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTGCGGACGAGCTCTGACTT[A/T]CTCTCTGTTCTGTCTATCTCTCCGCCACATACCA ACTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G C C T C	TGGCTCGCTG CATGCCCTTTA AGGATTAAGT	AGGGATCAA GAGAAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAAGAAACCCCTGGCCTCGCTGCCTC[A/G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCG
WI-15407	92 A G T T	CATGCCCTTTA AGGATTAAGT	TCTTTTCTCTT TGGTAGTGTG	AGCATGTAAGGAGCAGTTTATTTGATTGGTATATTCAGGTTTCTAACAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTTAA[A/G]CCACACTACCAAAAGAGAAAAAGATTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C A A T T	GTTGAGTATTT GTTCTGCTCAT	GGGAAAGGCTG GTACATATTGG	TCTGATGTCATTTATGGCACAAAAATTTCTGTATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTGTGCAATTAGTTGAGTATTGTTCTGCTCATAAATTTT[C]CCAATATGTACCAGACCTTCCC
WI-12326	25 G A C A	GACAGACTTC AAAAGCAATT	AGGTTTGA AAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAGCAATTCAC[G/A]CTTCCAGAATACAAAGTACTTAATACATATTTTCAAAC CTGTTTGCATTTCAACAAAGTTAGCGTTTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T ---	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGGATATAGGAATTTTCAGCATATGTATTAT[CT] TGAATAAATTTACAAAAGTGGAAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87 C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAGGAAAGGACAAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[CT]AGGGGCCACGGGAGGGTCCGGGAGACGACACTTTTCCCTGGG AAAG
WI-11321	67 A G T T T T	GGGAGGAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAAGCAGGGAGGAAAAATCCAAATAAATTTTTTAA[A/G]AAGGTTTAGCTATTCCTCCCAATGCTATTTAATACAATTTGAGTTAGGAGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40 C G T G T G C C C C A	GGATAAATCA TGTGCCCA	ATCAAGCTTTG GGCTCT	AGCATACTGCATCTCTTTTATGGATAAATCATGTGCCCA[CT]GAGAGCCCCCAAGCTTGTGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCTGTTCTTGTCC

WI-11352a	69	T C G	AGCAGCAG ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTCTGTTTCCAGAAAGGAGAGAGAGTCATCTACATAAGCACAGCACACATAGTGGAA AGTTCGCTAAGTGTCTCTACGAGAGGTGAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGGCA CACTTA
WI-11371	84	C T G	CAGCTTGGAG ATTCTGATTCA	GCCCGCCCTGA GCAC	TTAGCCCATGCTGTCATTTGCAATCACCTGTGAAACCTATGAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGTCGCTAGCTGCTAGCGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTTCGATCGGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCCT	GATTCATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTGGCTGATGGTGGACACAGAAGACTTTCATATTTCTGTTTAAAAAGTCT TCTTCAGTTCAGGAAAAAGGTACAGATTTAAAAAATATGACCATGACTAGATAGATAGAAATCAGC
WI-11388	88	C A A	GGTTATGTTT ACACGTAAC	TGCTTGTATC CAAGTTAAAT	TCATGTGCCAGTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTT AAATTACACGTAACTAAGTTCATATAATTTAACTTGGATACAAAGGCATTGTTATGCTAAT
WI-11392	55	T G A	GGTTATGTTT CTTGAACCTTA	GTACATTACAG TGTTTTGTAA	TTCTATCATTCCTTAAAAATGGGAGGTTATGTTCTTGAACCTTAAATAATCTTGCTTTTACA AAACACGTGAATGATCTTCTTGTGCAAGGGAACACTGAGTCTCGCTCTAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGT	AGCTTATTTG ATATTCACCCA	AAAGAAATAGATGGCAATTTGTTCAAGTTAAATTTGTTTGGAAATGGTGTTTATTTGATGGGTGAATA TGAAATTAAGCTTACCTCATCCACTCTAAAGGTAGTTGGTGAATTTTGAACCGTTGTCAAT
WI-11441	100	C A C	TCCCAACCAAC CAGC	TGCCAGGGCT TATTG	CTGTCAGTCTTCCCAACTAAACCGTGAATTCAGTATGCTGGCAGCACGCTGCTGTTCTTGGTG TATTCCTATTACTGAATCCCAACCAACGAGCAGTCAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAAATGAAT
WI-11466	26	C T T	TGAGAAGCCA TTTATTTTGCA	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTTATTTTGCAGTCCTTCAGTCCAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTGATTTTATAACAATAAACTTTCTATTATCTATTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G	---	---	TTTTCTTTTGTGCTCTTTTATAGTAGAAGCAGTGGTCAATAGTACCTTCTGTTGG TCCCTGTGTAGACAAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G A	GGCAGCAGG AGCAGAC	TGTACTGAGGA GCGGTG	AGGCAACACTGCTTTATAGGCGGGCAGCCAGGAGCAGACAGTGGTCCGCTCTCAGTACACATT CCCCACCCCTGCTGCTGCTCCCACTCAGGCTGGGATGGAGGGGCGAGCGTGGTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTCC	ATTGGAAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCATAGTGGAAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G	---	---	AATGGTCTGTTTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACGGTACAAAAATTACA GGTGGTTAGTTCAATACATGAGTACAAATCATTAGAGTCTTTACAAGTCAATAGAGTCTTTGGAT TTT

WI-14186a	52	C	T	A	GGTCATTGAT GGAAAGACAC	AACATAACCA CCTGTAATTTT GTACC	AATGCTGGTTTATTGAGAGCTGTTGGTCATTTTGGATGGAAGACACATA/C/TJGGTACAAAATT ACAGGTGGTTTAGTTTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A	G	GTGGGCTT	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTCAGTTCTAAACCTTGAGCTTGCAAGAGAACACTTGTGGGCTTJA/ GTTCAAACATGGAGTATAGGTCACCCACCCAGATTTCTAACTGGGTAGGCTGGGGTG
WI-12345	37	C	A	AAAGAGGAA	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGAA/CJA/CCTGAACCCCTCTGCAAGTATCTCT TTCCTGACCAGCTGGGCTTGGCAGCTTTGTGAGATTTGCAAAA
WI-13416	71	C	A	AAA	AAATTTTGG AAGTTTTTCAG	AGTGTATTATAG TTCAATGAATA ATTTCAA	GAAAGGCTGTAATTTTATTTTCAAAATTTTGGAGTTTTTTCAGAAAAAAATAAAATGACAAGAACA CATA/CJA/AAATATTGAAATTTTCAATTTGAACATAAACACTTAGCAGAGGAGGACITTTTGAT
WI-12310	46	G	A	AAAAGC	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGTCTT AAA	TTTGAAAAGATGCTGAAATTTATCCCAAGTATAATTTTAAAAAGCTTGA/JTTTGGACCCCAACATA TTTAAACATCTCTTACACATACAGAAATTTTCAAGTTTACAAATTTCCAGAAAGGCATTTTCTTTAAGCAG T
WI-12086	72	C	T	TTGGATT	CCGGGAAAAC TTGGATT	GGAGTCTCCG GTCTGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAAACTTG GATTTC/CJCCAGACCCGAGACTCCTCCAGTCTCACTGTCTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T	G	TTTTATG	GGCATAAAGT TCATAATATTG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTACAGGTGTATTTTGTAAAGATTTGTCTATCTAAATTTTTCATATTTTATTTGGCATAAAGT TCATAATATTTCTTTTATGATCTTTTAAATATCTGT/G/GGGGATTTGTACAGACTTTCTCTC
WI-11585	79	T	C	AAACAAAA	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTCC	TTAGAGGAAAGAAATAAAACACCGGTAAATGGGAAAAATCAGTTCAGAGGTAGGAAGAGCTGGGT TGCAAAAACAAAAT/CJGGAGTATCAGTGAAGCATGGCCTAGAAAGTCCAAAGAGCAGGGGTAGAGT TT
WI-11604	68	G	C	---	---	---	TTAGTTGGTTTCTCGAAACTTTATGCTGTTTATTTTAAACATAGGATGTTCCAGTTACCAGCATTTT G/CJAGAACTAGGGACTTTTCCATGAAAAATAATTAAGAGCTAAGGAATTCGACGCTCACCATTCTTC TTGTTACTCTGCAGTT
WI-11614c	108	C	A	---	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTCTCACTGTGAAACTGCAAC/CJA/JATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60	A	G	CAGCTGCTTG	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAA ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG/A/GJGG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83	T	C	---	---	---	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAATAAAT/CJT/ACTTAATAATAAGAAATTAGCCATACCACATTTGTTCCATTTGCTAC AAGAACAATTTGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCITTATT ATTAAGT	TTGATTTTACTAAGGCTCTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATAATTTTAAATAAATAATTACTTAATAAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAATTTGGCAATGA
WI-11627	23	T C	CCTTCCTTCC ATTGCTCTC	CATTTGCAACC CATCTCAAG	ACCCCTTTCCTTCCATTGCTCTC/T/CJCTTGAGATGGGTTGCAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATAGTATGCTCTTTTGTCTGGCTACTTCCATTGCGATGTCAAGTCCATCCATG
WI-11636	61	A G TCCT	GGACTTAAAA AGATCTGCTTA	AGAACTTGGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCTTAVGTA TATCCACATAACTCTAGTGTACATAAAATATTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCTCTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGTGGCAATAAGCAAACTGTGAGTAAACGAGGCGAGCTGAATAAATTTACAG TATACAATATTAGAGAATATTATGTGCAATTGCTCATCTACTCTGACCAATG/GJATAATCATCTTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C CTG	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTCAGCAACTG[G/C]AACTGTCTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTTCTGTGGTGTTCATCTACTCTCAGAGTTTACACTCATATTTTCATATTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A AA	AAGGAACTGC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAAG[G/A]CTTTACTTGAGGACAAAGCCTTGCTGCAGTTGTTT AAAATGTCTGAAACAATCAGATTCAGCCTGGAT
WI-11680	55	T C --		---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTTCTCCCTTTT/CJTTGCATAAA GGCTGGGAAGGTGTTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C AGGGGACAG	TTATCACAGC	GGCATTAGAGA AGCCAACTT	GTCCAAGAACAAGATACTTTTGACATCTTTATCACAGCAGGGGACAGT/CJAAGGTTGGCTTCTCTA ATGCCACCACCTTGTTGTTTCAGAACTTTCCACTTCGCC
WI-11702	69	C T CAGCAG	GAATAATACT GAAATAACCA	AGAACAACCT AAGCAAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTTCAATAATTAATAATCGAATAACTGAAATAACACACAGC AG[C/J]TTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAAATTTTGTCTGCAGA
WI-11706	60	C T TTCTCTTCTT	TGGCTGGAATT TTCTCTTCTT	ATCACCAAG AACAAATTCCA	TGCTGATTTCGCTTCTACCATCTGGCTGGAAATTTCTCTTCTTGTAATAATTTATTTGGCTG GAATTTGTTCTTTGGTGATTTGTCCTTCTGCTGCT
WI-11709	105	T A TTCAGTTTGC	AGAAGCTTGC	TCATTTCTTCT AATTTACGGG A	AATATCATCACTCATATCAGGGCATGTTTATAAAAATGAGAGATTATGTCTCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAAGCTTGCTTTCAGTTTGGT[A/G]TCCCGTAAAAATTAGAAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103	C A CAGTCTTCA	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACTGTCCCCAGCTTTCCAGCACACAGGACCCACACTCTAGACACGCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTTCAGT[C/A]CTCTCCCTCTCTCCACACACTCTCTC

WI-11715b	123 C T	AGGCTGGCTGC AGCTT	TCCCATCCTG TGCT	AGAATGGAGCTGTGGGGAGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTTAGCCAC AGGATGGGGACTGGGAAGA
WI-11715a	49 A C A A A	GCACACAATG TAAACACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTGGGGAGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTACGCCAC AGGATGGGGACTGGGAAGA
WI-11727	43 G C T C A C A	AACATCCTT AAAACAACATA	OCTGTGGTTG TGTTGCAG	CTGGATTTCCTATACCTAACAAATCCTTAAACAACTATCAACA[G]CTGCAACAAAAACACAGGC AAATGAAAAACAGATGCCACAGACAGCACCACCATGGCACACAC
WI-11728	16 C G ---	ATCTGTGGTT TCGCCCTG	---	TTTTATTATCAAACT[G]CAATTCCATTTCACAAATGTAAAGTTATCATCAGCTCCCCATCCACTTT CTCCATCTTCTATCTTTCCCAACCCTACACTTTCTCCCTACAAACCCGGTCCAAA
WI-11758	61 A G T C C C T G	GCCTCACAAA GTATTTCTAA GAATATAA	TGATGGCCCT GTGTCTA	TTTTCCCTTTTATTAAAGTCCGTATACCTAGAGGAGAACTGTGGTTTCGCCCTG[A]GTAG ACCACAGGGCCAAATCACACAGCTTCTGTAGAGACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37 A G A A T A T A A	GGCTCAGAGA GCAAGGGAA	AAAGTGCTCA TCTGTGAAC T	CCGGCCTCACAAAGTATTTCTAAATATAATTTGCT[A]GTAGTTCACAGATGAGCACTTTTCA CATTAGGTGATATGCAAAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93 T C ---	GGCTCAGAGA GCAAGGGAA	AAAGTGCTCA TCTGTGAAC T	AGCAGATGATATCTGCCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAAGAATT ATTATTGCCTCTTTTTCCTCCCT[G]GTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G C A A C C T C T G	GGCTCAGAGA GCAAGGGAA	AAAGTGCTCA TCTGTGAAC T	CATGACAACTCTTTATTAAATGGGCTCAGAGCAAGGAA[G]CAGACAAAAATTTACAGTCTGA GTTTTGGCGCAGAGACCCCTCTCCACCTTTTCATGCCTGTGTGTACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G A A C C T C T G	GGCTCAGAGA GCAAGGGAA	AAAGTGCTCA TCTGTGAAC T	TAATCAACCACTTACCAAACTCTGT[A]GCTTAGCCTGCCCTACCATGCTCAGAGCAC TTACATTAACTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61 C A A G T A T A C A	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACTTT ATAAAAA	TTTTAATCCCAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C]AAGT GATTTCTCTTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T A A G T T A A A	GTATTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTACTAATTTCCATTTCCTCCCTTTTATAGTTTTAATGTGTGATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTTCTA[C]TTTGACAGCAGATCTTCAAAGTTTGCTATAGACAATCTGA AAATGGGTTCTGAAT
WI-11906	52 A G A T C T G A A	TGTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTATAACATCAAAAGAAATCTGAAT[A]GTGAGGGAACCTG CAGAAATTAACCTTCAGTCTAATCTCAGAAATGCCAGAGTAGATGAACCCCTTTACAG

WI-11909	78 A	TTGTGTTGGG TGGTCAAG	CTCTCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTGTTG GGTGTCAAG/GTCTATTTCAGAAAATCTCAGAGGAGGACAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
WI-11806	60 T	CATGAAGAGT GGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTTCAT/GJGTT TTATTAGTATATAAATTTGGCTTTACAGGAAGCATTATGG CCCTAGTGAATACAACTTTGTCTCTGGAGAC/GCAGCTAGTCTAAGAAAACCTTCTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCTCTGGGAAGAAGGAA
WI-11946	31 CA	---	---	ACAAAATCACAAAGTACAACACTGCTTATTTTCTTGGCTTGAAGATCAGATCTCTGGTTTATTAA/T GJATCAACATTTACACAGCTGAAGGAAATTAACCTGAACCT ACCTATTTGAAACTGCAGAAAGGGCAGGACAAAACAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA/T/AATAAAAAATCTGTAAACATTTCTCTCATTTCTTACGA ATACCTCTTTTGATATGCAAAATCTATGGCATACACAGAGGACCTCTCAATGCCCTG TTCTGCTGAAGATCACAAAACAATTTCAACCTCTGTGTTCAAAATAATTTAAGGATCTTGTACCTTT GTGTTTATTTCTGTTTCAACTAAGGAC/TAGACTTCAGAAAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTTCATTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-11049	95 CT	---	---	CAACATTTATCAACATGGTAGGGAAAAAGTTCTCACTCTGCACATATAAAAAGGACAGCCAGATATCA AC/C/TGTTACAGAAATGAATAAGATGGAAAAATTTTAAACAAATTG
WI-15488	69 CT	ACAGTTAAT GAAACACATC CGT	TTTCCATCTTA TTTCATTTCTG TAAC	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTG/JGJGTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAACTTTTCCCAATTTACAGACAAAACCCAGT ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAAGTA C/C/TGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAAGTA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA AATCTTTATATTTCCAGCTGTTGAGACAGTATTTTGAGGGCTGATTTACCTCTAGCGCGGAAACC AGAGCCAGCTATTAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCAATTT/CJCTCTTTTAGC ACGTTCTTTGTTCTCTC
WI-13654	49 A	CGT	GGCTGGTGAAA TGATGTGAT	
WI-11070b	135 CT	---	---	
WI-11070a	110 GT	T	TTGGAGTACCT CTCTGCACC	
WI-12020	121 T	C	---	

WI-11076b	142	G A ---				CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTGGGAGGCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGGAGGAGCATGTGCATATCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCACACATTTTAAATGATGAGTCTCTCAAGGAACACTCACTCACTGTCAT G
WI-11076a	106	T C AGGCA			TOCTGCTCTGG GTATGTGAC	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTGGGAGGCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGGAGGAGCATGTGCATATCCAGAGCAGGAGAGAG GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTCTCTCAAGGAACACTCACTCACTGTCAT G
WI-14263	49	T C GGCATATTCA			GGTTATTCAAA AATTAGTATGG GACA	ACCTTTAAAGTTTCTCCACCTACTCCCGAGAAAAGGCATATTCAATCTGTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTCTACTAAGAGAGTTCTTTTGGCTACAAGTAACA AATTATGCTGAAATTAGGAAGGGAGCATCTGTAAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAAGCAAGTACCATTTTCCAAAGTATAAACTCGTA
WI-14267	28	T C ---			---	GATTTGTTTATTTCATCTCGCTTTTCTTTTCTTTTAAATAGAACATG/A]CTTTGATTTTATGTA TATGACATCATCATCATGAATTTTCTCTTACTTTGATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGATGAGTTCA
WI-13892	50	G A TAGAAC			TGATGATGCA TATACTAAAA ATCAAAAG	ACCTCTTCTGATGACACTTGTACCTGTAGGGGTCTAGAGAGAAAAGTAGTAGACTCTACTTTGCG TACAATTCAGGATGCAGGGCATGAGAGGATCCCTCTCTC]GTCCAAGGAAAGCTTTTGGC AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTCTTGTAAATCTGGAGCA[G/C]ATTCAAGCAGCAAAATTTACTGAACACTTGTATGTGCTG G
WI-13951b	88	G C ---			---	AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCAGATCAGAGGAAGAG ATGGCTTCTTGTAAATCTGGAGCAGATTCAAGCAGCAAAATTTACTGAACACTTGTATGTGCTG G
WI-13951a	39	C T CAAA			TTCTCTGATC TGGGTCT	GAGACCAAAAAGGCTCTGCCCATG]ATTTCCCGTCTCTCCCTCTGACTGACCCCAAGTGTCTT ACAATGAACATCCCTCAGCCCATGGCATGGTGCATCCCTTCTCTTGGGATCTGTGAATATAACCA ACTGCTTGTCAATGGC
WI-13264	25	G A TTGCCAT			GGAGGGAGAG ACGGGAATA	TTATTTGTCAATTAGCAAAAGGAAGTTAAATACTGATAGA[C/G]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAGTACTAACTTGTCTCACTGTCAATTTCCCTCACAAGGAGTTGAGCCCTTAGTGAC
WI-13960	39	A C TGATAGA			CATGAAAGGA CAAAATTTGCAT C	AACTCTTTATTGTTTAGCTAGCCCCCAGTGACTTTATGCATCTTATAACCAAGACCTTCAG[C/T]AG AGCAAGTCTAGCCAGAGGTTTATCACACTTTGTCTCAGGGTCCACAGGAACCCAGGTCTTGGCT
WI-15843	62	C T CAG			CTCTGGCTCAG ACTTGCCT	

WI-13983	52 G A	TCTCTCCCACT CCTTAAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCT[G/A]CCCACTGGGCTAA GAGAGTATTGTACAGATATGCACCTCACTGACTTAACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAAGATAAATAAGATGGACTTGCAGGTGTAAGGATTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGTATTCTCTGAT[G/C]TTTCTCTTGGCAACTATTCTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAGAAAGGCCCCGAAAATATGAGTGAGACTCA
WI-14284	55 C T ---	CCGCTGCTATT CCAGAT	GGTCTCTTCC ACCAATCTT	ATTTCAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAACA[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCTTGA
WI-14288	85 G C	TGATGTAGTTA CCCCACTAAT	CATAATATTGG AAGTCAGTGGT	ATGACCAGACCAGAGCCCTGTCTTATATGAAGACAAACAGGTGGCCATCTTGGTGGAGGGATA CCGCTGCTATTCCAGAT[G/C]AAGATTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33 C T ACAAC	CCCCACTAAT ACAAC	TCTATACACTT CTCACTCTCTT	TTTATTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCCTGACTTCAAATATTATGAGAG AAATTAATCTCCAGGGAATTTTTCAGAGAGAATAATA
WI-13529	42 T C TTACCA	CACAAACATT TATTGAACAG	GGTCTCTTCC GCTT	AAATATGATTCCATTCCACAAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCTCGAGGGTTTATAGTCTACAGGGGGAACAACCTCTC A
WI-13859	84 G A ---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAATTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTCAGGAAAGGACTCCTAGAACTTGAGCA	---	ACA
WI-13536	29 T C ---	TTGAAAGGATACAGAAAAAATCAGCGAAG[T/C]GAAAAGGTGGATAGCGTGAGTAGAGGAGAAAT TAAGCACCAGCTTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTCTCAGCA	---	
WI-13373	52 G A ---	TTTATTTGTTTGGTAGAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCTTTGACGCGCGGCCCTTGAACTCTGACATTCACAGTCAC	---	CGTAATAGAAAACAGAGCT
WI-13477b	61 A G ---	TTGGTTTTTAATACCTCTGTGGATAAAAGGACATTGTTTTTTCATTAGCTGTCTTCAA[A/G]GAC AGAGAAATAAGATAAATTACCTTAAAGAAAATAAATAGAAAATTAAGGAACATGTACCAAGGTGG	---	TTTAGACTCTCTCAGTT
WI-13477a	32 A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTGTGGATAAAAGG[A/G]CATTGTTTTTTCATTAGCTGTCTTCAAAGAC AGAGAAATAAGATAAATTACCTTAAAGAAAATAAATAGAAAATTAAGGAACATGTACCAAGGTGG TTTAGACTCTCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTTAGCATGCAATGCAATTTATTTCTGGCAATAAATTATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAGAT/AAATGTTTCTGAATGTGCACACTAGAATATATGCAGAAATCCTTT AAACAGTCGACT
WI-12229	89 T G A A A	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAATAATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAATTT/GJACCAAAAAAATTAAGATTTTTTGGGACAAATTCACATGTT AAAAAT
WI-13582	43 C A A G A C T G G G G A	TGCAATCTAG AAGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGGA/CATGGAATCTAAGTGCAGAG AAATCAAGACCGATGGTGAAATCTGGGCGAGCTTCAAAATTTCTGCCTCTCTAAAAACATTTTCAC CCAAATTTTCATTATTGGC
WI-13857	28 A G		---	TCTGAGTTGATAAAATGCTTTTCTGAAC/A/GTACATTTTAGGTATCTGGCACAATTAACCAATGT CTGCCATTTTGTAGCTTTCATACAGTACAGATTTTCATTGATGTCGCTCCACATCTG
WI-15809	77 T G T G T A A A T G C C	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAA	GTTTAAAGTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC/TGTTTACAAACATTGAATAGTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T		---	TAAATCAGTCTGTGTCAGAAAGAACAGGACTTGATCAAGCTTCCAGCCCTCACACTCTATCAGCA TAGCAATTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAAAACCAAGAGAAGGAA/ATJGGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G A A	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACTTA GCTGCAGTAATAC/TGJGCAATCCCATCCACTCTCTCTCTTTTGTACTGAAACTCTTCAAAAGAACT GCTGAATGCTCTCTC
WI-15801a	24 G A A A T G G G A A G C	TTTATCCAAAG AATGGGAAGC	TCATTCAGCC AATGAAATG	TCITTTATCCAAAGATGGGAAGCG/A/CATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACT CTAGCTGCAGTAATGCTCATCCCATCCACTCTCTCTCTTTTGTACTGAAACTCTTCAAAAGAACT GCTGAATGCTCTCTC
WI-13763	59 T C G C A G T G A T	GGCTGGACACT GCAGTGAT	CCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATTT/CJAGGG GCAGGTGTGGGGCAGGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48 T A A C C	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACC/T/JAGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCCCAACATTTGATATTTTGTCTTTTCCCGAGGGCAAAAGA GAGTCTTCCAGAAACCTC
WI-13789	62 G A A G G G A G	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCACATCAGTGAGAAAACTCAAGAAATTTGGATGGCTGAGGGAG/GA GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCTCACTCTCTT GAGGTCCCT
WI-13594	66 G A A G C	TTTTTAACACA GATCACAAAA	CCTTTCGCGCA GTACTTTT	AATAACAAGTTTAAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAACACAGATCAAAAAAGC/ GATTCACAAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATAGGCCAAACAGCTGC

WI-15625	40 C T ---			GTCTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[CTGTGTCCTCCACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCAACCAG	TCCCCACCCCA OCCCT	GTCTCACTTCTGTCTAGGCTGTAAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAAGAA[CTGJAGGGGTGGGTGGGAATACTTAATCAATATTTGTGGAAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26 G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACTTTAATGAGCCAGCATCCAT[GTJCCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAAACAAAGAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCTCT TGATTCCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAAATATTTA ATATTAAT	GATAGGAAAAGAAAGATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[GTJAAATCTATTAAATATTTGTCATGAGGTATGCACCT GOCA
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACTTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTACAAATATTTTAC TTTTAAAC[GTJAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CAATTCAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[CTJACATGCAACAATATAGATGATTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G AAA	CAATACATTT GCATTTTCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAACTGTAATCAATACATTTTGCAATTTTCTTAAAA AAAGAAGACATTT[GTJTTTCAAGAGAAAACTGTGGTATCATGCAAGAAAAAGCAGAAAAAATTT
WI-13909c	93 A T ---		---	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTCCCAAGTGAAGTTTCTTCTCACACT CTCTTCAAAC[GTJAAATATCTTTTTCAGAGATGCTAGCTAGTACCCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTCCCAAGTGAAGTTTCTTCTCACACT CTCTTCAAAC[GTJAAATATCTTTTTCAGAGATGCTAGCTAGTACCCCACTGCAACATCTCTCAA
WI-14323b	86 C A ---		---	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCATTTCTGGAC[CTJATGGGAACCTTGAAAAAGGCATGGCAGTGAGACCAGTA
WI-14323a	78 T C ACATCA	ACAGAAAAAT TAAGAATCAA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCAT[CTJCTGGACCATGGGAACCTTGAAAAAGGCATGGCAGTGAGACCAGTA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACACTT	AAAAATTGACAAATCACTAGCTGCTTTTGTGCTTTTGGAGAGACTACCATTATTCAAATTTATTATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[GTJAAAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTG	TTTGAATAATG GTAGCTTCCA AA	AAAAATTGACAAAATCAACTAGCTTGCTTTTGTGTCG/AJTTTGGGAAGACTACCAATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAAGAGTGTTGGGAATCACTCATCTGTGCG TGTAATCTGCTTACAGTCCCTTGCAAGACAGACATATGTTTTGCATAAAGATATAAAATTTGCTTCAT TTTAAACTAATTTAGTGTTT/CJTAAATTATGAACCTTTTGGTGAATTATGAACGTGTACCAAAG C
WI-15747	88 T C AGTGTT	TGCTTCATTT AAACTAATTT	CATAATTCACC AAAAGTTCATA TAATTT	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATACTTGGCTTGACAC/CJTGACACCTTTTACG GAGGGATTCCGGACAAC
WI-13752b	117 CT ---		---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATACTTGGCTTGACAC/CJTGACACCTTTTACG GAGGGATTCCGGACAAC
WI-13752a	106 T C AGTCTGGA	CCCTTCGTGA AGTCTGGA	COCTCCGTAA AGGTCTCC	AATCATTTAATGAATGTTCCAAACACACACCTTCACTGGGTACAGGTAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACAGATACATGATTACT/GJGGGTTTCCAGAAATCTGGATAC TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACAGTAATGGAACTTCATGCAGCTTTAGAT TTCTTTGCCAGCTAGGAGCTTGTTGATGGTGTGCTGAACAAACTGAAC/CJTGCTGTGCTTATCTTTC CTGATTCT
WI-13744	115 CT AAACTGAA	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	CCCTTGACTATATTGTTTTCCAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACCTTAT CJTTAACCATTTTCATCCACCATTTGTAAATCTCATCTCTCTGGGTCTGGATCTCAAAAACAGAT TTACAGTTGGATTAACTACCACACTGAATATACTGAATTAACCTTCAACCTTTTCATCCATTGAG C/A/CJAATTTAAACTCTTGCCAAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-15719	69 A C CATTGAGC	ACCCTTTCATC CATTGAGC	TGATAGTTGGC AAGAGTTTAA ATT	TAATCCATCAATCTAAATCACACATACATAGATCAACAGAAAGTACCACAGTATGCTTTATTTTGCA GGTATTAATTGGTTCTCTAAATCGATACATCCAAAACCTT/CJAGTTAGCAGCAAGCATCAGTTCTTC
WI-13810	106 T C AACTT	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	GGATTTTATTACATTAACTTGACACAGTTAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA TCAAACTGCACACTATAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC/GJATTAGTGACACATAGCTGTACACACACAGTG
WI-15736a	27 GT CACA	ATTTATTAC ATTAACCTTG	GTCTTTGATA TGCTGCTTAGT TTT	TCAAACTGCACACTATAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC/GJATTAGTGACACATAGCTGTACACACACAGTG
WI-13785d	72 GA ---		---	TCAAACTGCACACTATAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGAC/CJCAAATG AACAAAGTGGTAGTGACACATAGCTGTACACACACAGTG
WI-13785c	56 A C ---		---	

WI-13785b	40 C G ---		---	TGTTGTGACAG CTATGTGTCAG T	TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACAGTG
WI-13785a	27 T C TGCTT				TCAAACTGCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACAGTG
WI-13793	88 C G ATAGG			GGCAGGAGGA TTTGTACT	AGAAACCAAGTATATCATAGGCAAAATAAAATAGTTTTACCCCATTTGATACACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCATAAATCTATGACTTG
WI-13794	52 A G TTCTTCTC			AGAATGGGCTC TTAACCTTGTA	TAGTCTCTACAAATCCTTCAATCCATTTCTCTCTCACCCCTTTCTTCTC[C/G]TACAAGGTTAAGA GCCCATTTCTCAACAAACAAAAACAACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC			CTTGAACCAT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/G]GGCACCTTTAGAAAGAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAAGGAGGTAGTCCCTGTTTGCAGCCCCGGGCTGCTCATTTGTTA
WI-13424	66 G A C			TTTTCTCCCG AGGTCTA	GTCCTTGCACAAAGTCTCCCAACTGGTTTGAGATTTCCCTTCTGAGGTTTTTACCCCTATTCTT[C/G]A TAGACCTGGGGAGAAAACACACATGTGTAGTGCTCAGGACATGAGCAGGCCGCTTCACAAGAT GCTGGCTAAGGGCTTC
WI-14065	29 T C AATT			CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTGACAGGCAATTT[C/J]GAGATCCAGATTCAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTTCTTGCTGCTTTTAAATCCTGAACATTTTGAAGCAGGAA
WI-13446	22 G C TCACTCATCA			AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTCACTCATCA[C/G]CCTTCTGATTTGATCCCTTCTGCTCTGTAAATTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATCTGGTTTTGAGAGTAGTGAGCCCTTTTACTTTTT CTGACTGCCCTAAT
WI-13725	56 A C TGGGTGC			CCTGCTGTCTC GGGC	TCACACAAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTACAAAAACTTGACCAGGCAGGTTAGAAAGCAAGGCATGGTTTCAGGATG
WI-15702d	107 T C ---			---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAAT[C/J]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ---			---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAAT[C/J]TGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ---			---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]TGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

5

WI-15702a	48 G C A A A G	A A C A A A A T A A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A T G T T T A T G A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A G [G/C] G G G T A A A G G G G T G A G G A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A A C A T A C T A A T G G G T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113 T C ---		---	T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T C C A C T G T A T C C T C G G G T A A G T T T C C T C T C T G T A G A [G/C] G T C T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C ---		---	T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A T C C T C G G G T A A G T T T C C T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A ---		---	T G A T T G A G C T T A G A A A G G A A G T C A T G T T G A A T C A G A G A G G C C A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G ---		---	C A C A T T T C A G C A A C A A A T C G A G G T G C A A C A G G G T T A T T T C A C A T T A A T A T A T T A A C T G G A T T T T T T G T C A A T A A A T A G G A [A/G] T T C T C T T T A A A T A A C C A T C T C C T C A C T T C A T G G C C A G T A G G C T G T T T T G A G G C C T G A G G C C C C A C A C A T G A C A C G T A A G A C T G T A A C C A T G T G C A T G T G A G T T A T G A C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T G C A A G A	A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A A G T A A T T A G G A A G A G C A A G [C/T] G C A G T A A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C A G A C T T G A G A G C T T A A A C A A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T A A G G T T A A G G T T A C A A G G C C A A
WI-14085	31 A G A A A A A	C A T T T A T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T A	T G C A T T T A T T T C A T G T G T A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A C A A A A T A G C A T G T T G A T T T A A G T G A A A T A A C A G A A C A G G A G G C C T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T T C T T	G G G T T C T G A G G T G A A A G A A A A A	G T C A A A G G T T G C A A A T T T T A T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T C T A A A T T T C A C C T T A T T G T A A G T T A A A T A A A A C T C C T A T T T C T T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G G A A T G A A G G A G G G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G A T T T G A C G A C T A C A G C T C C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A C A G A G A A A T C C T C A T C T G G G T T G C C A G A C A G

WI-14379	102 C T	TCTATTAA GGGTTATGTC CACC	ATCATCTGTT TGAGGTGACA	TTTATGCTGTTGTTTCTACTGGTGGTCTGCTCCTACTAATATCAATCCTAGTAGTATTTCTTT TACTTGTGCTATTAAACAGGGTTATGTCACACC[C/T]TGTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAA[A/C]A[C]CCACCATTAAACAGGAGACACTGCAGAGGCTTATGTACA ACACGTGTCGCCGAGGCTGGCGAGGACTGCCACTCCTCCTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A	---	---	ACCGCAGAGCTGCTGTATTTAA[A/A]G/JACAAAGCGTCTGATCTCTGCAGGGCTGGGACCACTGC AGTGGGGCTCCGGCACTGCTCTCTCCAGGACTCTTCCACCACCCC
WI-15937	24 A G A	CGCAGAGCTG CTGTATTTAAA G A	GCAGAGATCCA GACGCTTGT	TGAAACTGAAACGTATTTCTCTCCA[A/C]ACACCGTAGAACTTTAAAGCCGCAAAAGACTCACACCC ACCACCTAGCGGCAAAAGGAAGTTTCAGGTGATACAAAGATGCTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A	AACTGAAAC GTATTTCTCTC C A	GGCCTTTAAGT TTCTACGGTG	ATGTTTATGATCAATTCOAACATACAGTACAGGGAAGGTGAAATGAGTAAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACAAAGCTCAGTCACTAC
WI-14124	92 A G	---	---	GACAAAGAGGAGCTTCTGTAGTCCAGCAGGCGCAGAGAGTTATCAGAACGGTGGTTTGACCT GCATAGATTTTTCAGGACTA[C/T]GTGGCCATGCCATTCTGTAGTGAATTAATGAACA
WI-14125	88 C T	GGTTGACCTG C T CATAGATTTT G C C A C	GGATGGCATG G C C A C	GTTTATTTCTCACAGTCTCGAGGTTAGAAGTCTGAGATGAGGATATCACAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGCTTTCACAT[G/A]GCCCAAGAGAG AGAACAAGCTCTCTGGT
WI-14136	120 G A	ATGCTTTCACA G A	CTTGTTCTGTC TCTTTGGGC	TTGTTGTTGGCACCAGAAAGCT[C/T]ATGTTCTATGTTATGTCACCTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-14138	23 C T	TGTTGGCACCA G A A A A G C T	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTATTCTAATAATTTCAAACTTGAAGCAACCAAGATGCTCTCAGTAGTAGTATATTCA GACAATC[G/A]AATAATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74 G A	GACAATC G A	TAATAIT	TTTTTAAAGAGTGCCTTCACATCATTTATATTGATTGCACACAACTTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTOOC
WI-15953b	59 C T	---	---	TTTTTAAAGAGTGCCTTCACATCATTT[G/T]ATATTGATTGCACACAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTOOC
WI-15953a	26 T G A T	TTTAAAGAGTG T C A T C T G T C T T C C T T C A C A T C	TCATCTGTTCT TGTTGTTTTTG A	TTTTTAAAGAGTGCCTTCACATCATTT[G/T]ATATTGATTGCACACAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTOOC

WI-14631	82	G A	---	---	TGAATTCATGGACAGTTTGGCTCTGTTTAGTGAAACCCCTCAAGCACTCTGCATAGTCGGCTTTCTGTCTCTTTAAAG[G]ATGGCTGGTCCCTCTGCCAAACTTTTAGGATTGGCCCTCCTCAGGGCCTTGTOCTGA
WI-6053	24	A G	---	---	ATCACCCCGTGTCTAAGAACAAAC[G]GTCCTTCATGTCCAACTCATATCCCGGGACTTTGTCAACTGCAGTACACTTCTGCTGATTTGAACCTGGCTTCTGGAGGAAAGCCCTCTAGAGCCAGGTAAAGGGGGTGCAGCAGTGAGGGGTATATCTGGCTGGCCAGTTGGAACCCAGGAG
WI-15964	99	T A	CTGGAGGTA	GCTCTCTGTCC	CAGAAAACCTCTTCTGTGTTAATAAGCTGATGCTAAAGTCAGAGCAGTCCAAAAGCAGGAGGCTGCCTTTGGGAGGTAGTAAGCTCTCTGTCCCTGGAGGTA[T]A[GCAAGAGGGTGGAGAAGTCTTGGCAAGCAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAAAATACCCATCAGAGACAGTGACAAGAGCAGCTGGGGGCACGGGGAGG[G]A[GAAAGGAAGAGAAAGAGGGGAGGAGCCT
WI-12075	103	G A	GGCAC	TCCTCTCTTC	TAATTTAAAAACACGCCCTTCCACATAGTGCCTGAGGCATCTGCACATTTTCTTAGAAGGACATGAATAGTGATGGAGGTACGGTGGAGGTCA[G]A[GCATCTACAGGGTCACTCGAGGAGGAACAG
WI-12179	96	G A	TGGAGGTCA	TGTAGATGC	CACAAATAGTGAATATCTGAGCAAGAATCATTTCTCATTTAAAAATTGT[G]G/AAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAAACCACTGTTA
WI-14651	49	C G	ATTGT	CTTATTT	AATGTGGACTTTCAAAACAAGGGTTTAAACTAATCTAATAACAATCTTACAACACATCCAGAGCATTATAACAAGAAATTTTACAGGCAGCTAATGTATTAA[T]A[AACCATGAAAAGAAAAAACTTGTATCTAGATGTCAGCAATGGGCTGAGACTGT[C]T[G]TCTGGTAGATGCAGTGTGTATGTCTTCTAC
WI-14666	105	T A	---	---	TCTATTACAAAAATTAAACAGAAATATGGCTTCGGCTTGTGCAAAATGTTTATATACACAGTC
WI-13473	31	C T	---	---	AAATTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAAAGATAAAATATGTCTTACAGAGTCATTTAAAAATAAAAGACTACAGATACAGGAATAAAAA[A/C]CACTTTTAGGAGATGAAAACACAAA
WI-13967	103	A C	AAATAAAAA	TG	TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCT[G]/A/AAA
WI-14408	60	T A	G	TTACTTT	TTTGTGTTAAGAACACAGCATTTTGAAAATAAAACCTATCTGCCATG[C/G]TTTACAGCCTTTTAAATTTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13683	47	C G	---	---	TTAGAAAACTGATAAAGCAACACAACTTTTGGGAAAGCACCATGGCAGTCCTTTTGTGCTA[C/T]GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-13910b	63	C T	CGTCT	CAC	ACATGGCAGATACAGAGCTGT[C/G]ATCTTGAAGACCACCACCTGACCAGGAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCGTCTGGAGCGTTGAAGGGTGACCAGC
WI-14635	22	G A	---	---	ACATTTGCACATGCAAAA

WI-16002	59	T C A G A A T T T C	G A T A A C A T A A A A T G A T C A T G	G C C A T C T C T C T T T G A C T T T T	C C A A C A T T T T A A A C C T A T G A C T G G T C A T T G A T A A C A T A A A A T G A T C A T G A G A A T T T C A T T C J G T T A A A G T C A A G A G G A G A T G G C T A A T G A T G C T G G G C T
WI-15361b	101	A G A	C C C A C T T G A A C T C A A G T C A T C	C T T T G T G C T A A A A	G T G G A A T T T T A T A A G C C A T C A A A A T T C C T T C A C A C T A A T A C T G T T G A C A C A A G A T A A C A C A T C T T C T T G C T A C C C A C T T G A A C T A A G T C A T C A J A G J T T T A G G C A C A A A G G T T T T A G T T T T C T C G G G A A T C A A G T T T A A C C A
WI-14759	73	T C G T G C G G	G C G T T T G A C T T	T C C C A C A C T G C C C C C	T G A G T T A C A A C A A T G A G C A C A A G T T A G A A A A T T G G T T T T A T T C A A A C T T C C T A G C G T T T G A C T T G T G C G G J T C J G T A C T A C A A T G G G G G C A G T G T G G A C G G G A G G A T T G C A A C C A G A G T T C A T A C T G C A A
WI-12535	50	A T T A T	C T A G G A G G T T G A G G T G T A G A	G C T C A C G A G A A G A G A G A A	T C C T A A C A T T A T T C A G G T G G T A C T A G G A G G T T G A G G T G T A G A T A T J T C T T C C T C T C T C T C G T G G A C C T T A C T G A A G A C A G A T G C C G T T C T T G T T A T C A G C T G A A G G C A G T C T C G C C A T C T T A A G A C C T G C C C T C C
WI-13805a	112	G A G G G A A	A A G G C A C A C	C T C A G C C T G C C T T G A C C	T T C A T T C A T T A T G C T T G G C T T A C C A A T T T T T A T A G C T A T T G G G A G G C A G A A A G G A A T T T T G G C C C C A A A C C A T G A G A T T G G T C A G A A A A G G C A C A C G G G A A J A J G G G T C A A G G C A G G C T G A G A G T C A C A T T T C A G A C C T C
WI-12340	18	T C ---		---	A C A C A A T A A T T C C A T T J C J G A G T G A T T A A A C C T A T T G T T G T T A G A A C C A A A A A A A C T A C A A G A A A C A T T T C A A A A C C T T T T T T T C A G G C T G A
WI-14808	52	T A C T A C C C T G T	A C C C A C C A C A C T A C C C T G T	A T G T T A A G A T T T T	C T T T G A A C A C T T T A A G C A A C A G T T A A A A G T A C C C A C C A C A C T A C C C T G T T A J A A A A T C T T A A C A T T G T G A T G C C T C T G C A T C A A T T T T A G A A A A C A A A G A A A C A C A A C T G A A G G C C C C A T G A
WI-14816	29	A T ---		---	A G T T A A A A A A A T C G A G T C A G C A T T T A T J A A A A A C T G G A C A C G C T T C T A T A T T G C A A G C T C A T T C A A A T G C A T T A T T T T G T A T C C C A A G C C C C T G A A A C A C A T G A A A A A A T A T T A C T A A A G G A A T G T T G A T A C C A G C T A C G A C T T T C
WI-12542c	71	G T ---		---	C C G T G T T T C A T T G A A G G C T A T T A G G C A A A C T G A A C A C A T T A A A T G T C A T C C A T G T G A G G G C T C T A G A T C A T G J G T T A G G T G A T T G A T A C A A A T A C G A T C C A T A A
WI-12542b	70	G T ---		---	C C G T G T T C A T T G A A G G C T A T T A G G C A A A C T G A A C A C A T T A A A T G T C A T C C A T G T G A G G G C T C T A G A T C A T J G J T A G G T G A T T G A T A C A A A T A C G A T C C A T A A
WI-12542a	45	C T T T T A A A	G C T A T T A G G C A A A C T G A A C A	T C T A G A G C C C T C A C A T G G A T	C C G T G T T C A T T G A A G G C T A T T A G G C A A A C T G A A C A T T T A A A T G J C J T A T C C A T G T G A G G G C T C T A G A T C A T G G T A G G T A T T G A T A C A A A T A C G A T C C A T A A
WI-12173	57	C T C A A A A A	G G A T A C A G C A G T A A A G A A T A	C C A C C T C T A G A A T G T A T G C T C T	C A C C T A A A T C A T T C T A G A A A C T G G G G A T A C A G C A G T A A A G A A T A C A A A A A A A A A T C C T G C J C J T T A T A G A G C A T A C A T T C T A G A G G T G G G A A G A G G C A A T A A A T A

WI-14836	28 T C ---			---	TC TTGGAGGATAGAGGACAGAGTGTTC/GTTGATTTCGTTTCGGTTTCAGTTTGGTTGTCATT GGTTTTGTTTTTGTCTAATTTTGGCCACCCCTATAAAAGCAGTGCACCCAGAGGCAG
		TGGTGACAG		TTTGTTCGTA	ACATTTCCCTTATGATAGCAACAATAATATGATGGTGGTGACACGGAAATACCTTAATATTTAA
		GAAATACCT		CTTTTACAAA	AGTTTGTAAAAGTAGCAACAAAATTTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA
WI-14856	60 A T A A			CTTT	GGCTATAAAAAGCTCCAAA
					ATGGCAATTTACTTTTATAGCAATGAACAAATTTGTCAAAGGGCAAAATTTTTTGTCTG/GA/JAG
WI-14863	61 G A ---			---	TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCCTATTATTGATTGCCACT ACCTGGC
		GACATCCAA			TTTTAATTAACGTAAAAAGGCAGGACATTCCAAAGGCTCTCTAACA/T/CJGAGTGTCTGCAGGCCCA
		GGCTCTCTAAC		TGGGGCTGCAG	TTGGCTTTGAGATGTGAATGTGTTAACCCAGGGTGA
WI-14867	46 T C A			ACACTC	ACGGAGTCGTCCTGATGTATTCTGTCAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAAAT
		CCAAATTGAC			AGAAAAATCCAAATTGACAGATATTCTGCA/GA/JAATAAATGGCCTGACCTCATCAAAAAACATCA
		AGATATTCTGC		GCCATTTATT	ATGTCATGAAAAACACAAAA
WI-14733	98 G A A				TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATAGGTGCCACTAAGGAAA
WI-14898b	79 A C ---			---	ACTTCTCCAT/CJAAAGCTGCCTGCTGTGCACGTTGCCTGGCTTTGCTAACCCCTGGTGTGCTCATCT GCCTGTGTTCTGCTT
		CATGTACAGG			TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/CJAGGTGCCACTAAGG
WI-14898a	50 A C A	AAGAGTTGCT		AAGTTTCCCT	AAAACCTTCTCCATAAGCTGCCTGCTGTGCACGTTGCCTGGCTTTGCTAACCCCTGGTGTGCTCATC
				AGTGGCACT	TGCCGTGTTCTGCTT
		GGCACACATT		TCGTCTGCAAG	TGGTATTATTTCGACATTACTGTAGAGGCACACATTGGACTCTGAC/GA/JATTCCCTTGCAGCAG
WI-14907	48 G A GGACTCTGAC			GGGAAT	ACATTTGTGAAGCTGCTGGTGGGCACACCCCATCAATCAGTGCCTGCTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
		CCAATACATT			CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCACTTCCTGGT/CJAJAAGGTCTTTTC
		CAGTTCTCTGGT		CAAACCAGGA	CTGGTTTGCAGACAGATACCTTGTGTATCCTCAGATGGCAGAGAAAGAGAGGAAATATCT
WI-14911	52 G A C			AAAGGACCTT	CTGATGCTTTGACATCTGGGGCATTTGCTGTCTAGAGAGACTACTTCTCTGGGACCGCAATTC
					TAGTGATAGTAGGACTCA/CJ/CCTGCACGTGCACCTTTTATATACAGATCAACCAATCCAAAAC
WI-14913	88 C A ---			---	CTACACCTCCAACACCT
		CTGGACACAG			
		TTTTCTCTAGC		CAAGCCCAGGA	ATTTCTTGTATGGCTGTGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTTCTCTAGCA/G
WI-14914	66 G C A			CAATAAATTC	CJGAATTTATTGCTCTGGGCTTGATGGCTTTCACAG
					GTTTATTTCAAATGACACATCCAGATTGAAATGGGCACCTTAGCGAAT/CJACTTGTGGACCACA
WI-14926	49 T C ---			---	AGACTTGCTGAGAACATGTTCAAAGACAGTTTTCAAATAAAAAATTTTCCTTAATCAGGTCCA

WI-16083	89 C T	ATGTTTAAACA CAAACATATC AAGGAT	TGAAAAGATT CCAGCC	GCATCTTTATTACCACAGAAACTCATTATGTCTTAAATCAATGTTTAAATATAAAGCATGTT TAACACAAACATATCAAGGATC/TGGGCTGGAATCTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCTTTTCCACAGGAGGAGTCCCTCATGGATC/TJGCGGTATTG GTTGGTTGGTGATTGGGAGCAGCAGGGAGAGCAA
WI-14946	47 T C	---	---	TCAATCTGAAGGTGTCAAAGTGGTCTATTGGCCCCCAGACATAACA/T/CJCTCTAAATCATCCTCTA GATCAGGGAGTCATAAGGACCAATTAAAGGCTCATTACACACAGTACTTTATGGAAAGGATT
WI-15987b	80 A G	---	---	ACATTAACACAGCACAAATTAAGGGTCCCAACGAGGTGGTAGTGCCTCCACTATGTGAGGACAC TAAGAAGATGGTCA/TGCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32 C T	CACAAATTA GGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAACACAGCACAAATTAAGGGTCCCAACGAGGTGGTAGTGCCTCCACTATGTGAGGA CACTAAGAAGATGTGATCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56 T C	AGGGAACCTG CTAAGTTGTCA G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAGTCTTATTGCCGTTCTTCCAGGGAACAGGAAACTGCTAACTTGTGAGT/CJCTCAACA ACTGATGAAGATCATCTTCTGACCATAGCGAACCTGTAAAGGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAAGCTA TTTCTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC/TG/GTAATATACTG TTTTCTGACATTCCTGTTATCAACTCTCTGAAAAATC
WI-14958	83 A G	AATAATTAT CTCTTCTTTT CAAGGG	AATGCATTGAT TTGGGTTTT	GTGATTGATCTGTAATTATTGGGATTATTATTCAACTCTAAAAATCCAGATGAAAAATAATTATCT CTTTCTTTTCAAGGG/TG/JAAAAACCCCAATGAATGCATTTTTCAGTTTCTCCAGGCTTTGAAGCTGC AGCAGAAAAATCAAGGA
WI-14978	35 C T	GTTGATTGCT TCAGTGGTGT TATTGGATTTT	TCAAACTAAAT CTTCCATTGTA AGC	TATTTTTTAATTGGTGAATTTGCTTCAAAAG/C/TGCTTAGAATGGAAGATTAGTTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGCCACAAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTTT T	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTGAGTGGTGTATTGGATTTT/TG/JTTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTTAAATCATGCTACCAGCCCCATCTAAGCCAAATTCAAACACCACTCTGCATTA AATGAAGCTGCAG/C/JAGGAAAGCTGAGCACATAGCACCCCACTGATCGGAAAAAGAACGTA
WI-15002	72 T A	---	---	AAATCTCTTCTTCCACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAAATGCCTCTTGA TTTCC/T/JTTCAGTTTAGGCTCAATGGGCTCTCCTCAAGGCTGACCTCAAAAGGCCAGTT
WI-15000	90 G A	GACAGAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAAGTA/G/JTGAAGTTTGTGACAGAACTAGAAAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACCT CATGTACCTAT GAAATAA	CACTGGACATA TTCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACCTTTCATGTACCTATGAATAA G/AJACAGGTAGGGAATATGTCAGTGCAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T	AAGGACGAT TATGATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTATTACAGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTAGTATCTAAACA/AJTCAAAAAACACTGGGACATGCCCTTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A T	CCTGCCCTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTGTTGTTATTAGCACCTGAATTTAGGCAAGAGAAACATTTCCTCTGAAGACTCCATGCAGT CAAATTCCTGCCCTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGCACTCAGOCCTC
WI-14712	38	T A CA	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA/T/AJCTCAACAATACCATATACAACATACT TTCAATCACAACTCAAATATAAAATAACCTACAAAAATCACATTGC
WI-13712	40	A C T C T A T T G	TTTACTTTGTT GTCATTTTAT	CCATAAGGTCT CACACTTTCT TAT	TGGGATACCCCTTTACTTTGTTGTCATTTTATTCTATTG/A/CJATTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGGCAATATGCAATATAATATTGTGTGTTTAAATTTATGCAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTACTCTGGTGATGCAATTGAAATAA/C/TJATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAGTTTAAAGAGGACTATTCTTTAAACAAAGACAGTGTGACATTATTTCAGGT
WI-13453	88	T A TC	AATGCACAAA ATCTTGCTCT	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGCATTTGAGTCTTTATTATATTGGGAATTGCAGTGATATTAACTTTGTACAAAT GCACAAATCTTGCTCTCTC/TJATGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGCTCT AATGAACCTCATTGTCCAT
WI-16167	58	T C G A T T T T	CGCACTCTAA ATTAGAGATA	TGCTGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTTTCTGATATACATT/CJCATCTT ATTCACCACGAGCACACACACGACAGTAGAACAGTTCCACACCTGATAAATTGCACAAGATG
WI-14482	17	G A ---		---	GCAGAACCAATTAAATAA/G/AJAATCTGCAAGTTTCCCAAGAAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGATAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---		---	TGTAGTCTTCAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTATTCOCAGTATCATGTAC GCCTAAAAAAAT/CJGTGTGCTTGTGCTGCTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C C A G A G T G C	TGAAGATTAA CCAGAGTGGC	AATTGTGTGCA TTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGATACTCTATAAAACCAACCCACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTGG/CJCTCTCTCAAATGCACACAATTAAGACG
WI-15012	59	G T A T G T	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTTCATTGAAGCTTTG/TJACCT TACTATCTAGGCTATTGGAGTGTCCCCAC

WI-15100	74	G A ---			---	TCCTATTACAGCCAGAAATAACCCAAATTATTTCCAAATAAAGCAAAAATTGGAACAGACTGGA GTGAGAAACG/AJGGTTCCACACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTCTAGTGGACTTTAT
					GTCAACATGTT	TGGTACAGAATGTTTAAATACAGCAGGGCAGTGATCCAGTTAAATAAAATTAACCTTTATTTT CCCAATATAAAATTAATAATTAA/AJTGCTTAAAGAAAATAATAACATGGTGACAGCTTT
WI-14492	92	A T AATTACT			TAAGAC	TCCTTAATTTTATCGGAATCCAGGACACACAAGAAAACACCCAAAACACATGGAGACAGAAG ACGAGACAACTCCTCCCCAC/AJGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002c	89	T C ---			---	TCCTTAATTTTATCGGAATCCAGGACACACAAGAAAACACCCAAAACACATGGAGACAGAAG AC/G/AJAGACAACTCCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68	G A ---			---	TCCTTAATTTTATCGGAATCCAGGACACAA/CJ/AJAGAAAACACCCAAAACACATGGAGACAG AAGACGAGACAACTCCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30	C G GGACACAA		TCGGAATOCA	TGGTTTTGGG TGTTTTCTT	TTTTCATTATTTTCCAGAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAATTAACCTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAA/CJ/TGTCATATAATAATATTCATATTCAGGATTTTG TGAAATAGGTGATTGGGA
WI-15116	96	C T GTTCAGTAA		GGGAGCCCTA	CCTGAATATGC AATTATTTATT ATGACA	GCAAAGCAAAGCTATGGAGCCCTAAAGGAATGGGA/CJ/TGTTGGTGGTCGCTTGATACTTGGT GCTTGTCATGGAGCAGAGAGTCTCCTGTCATGCAGGGGCGTCACATATTTTAACGCACTAAT TTGGGCAAACTGTCATTC
WI-12578	37	C T AATGGGAA		GGCCTAAAGG	TCAAGCGACCA CCAACAG	ATTTCACGTTGGCCAGATCTCCCTTATGTTGGCATTGCA/AJAGACACTGCACCTATCTGAGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTACCATTTCTAA CCTTTGCTCTCTGAACCTGGGACCAAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTAGAATCAAATGGG/CJ/TGACTTTTCCCTGTTGGTGGAAAACCTCTGTGAGGGTTTGGCA
WI-15153	40	A G GCATTGCA		CCCTTATGTTG	AACCTCAGATA AGTGCAGTGT T	AGGAAAAGAGTGGTAAAGCAAAAGGCGATCATTTGGATGGAATGATTATGTGCACGACCTTGAGGAC CTAGAAAAGCAAAAC/CJ/TGGAGTGATTATGCCAATCAAATTCGAAGGTTGGAGATATGCTAAAA AATTTGCTAGTGCAAATGGACCCAGAAATGGAAGGGCTATGTAACTACACA/G/ATATGCACACCAC AGCCATGTGTCAGTGCACAGATCCTCTTGTCATTCAGCTTTCTTAAAAACACATCAAAGGCTGCA
WI-15215	84	G C TCAAATGGG		TGGCTTTAGAA	CCAACAGGGGA AAAAGTCA	
WI-15225	80	C T C		CTTGAGGAOCT	TTTGATTGGCA TAATCACTCC	
WI-15152	51	G A ---		AGAAAGCAAA	---	
WI-15123	55	C T TAGGATG		TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAACAGAC	TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG/CJ/TGCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAAAACGAGATAAAACACAAT

WI-15182	49 C A	GCACAAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACCTAGCTGCACAAACCAGGGCAAAATAC/ATGTCTGGATTAAACCC ATGCTAATGGGTACCTTTATTTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38 T C	GGGCCCTGGC ACTATG	ACTATCCGTC AGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTGGCCCTTGGCACTATG/C/CTACTCTGCCTGACGGATAAGTTGGC ATATGGTTACAGATTGCTTGTCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42 T C	CATTATTGAG TATTCTTGCTT TGAT	GTGTAGTCTT ACATGCTTAGC TAGAC	TCAAGTGGTAAATAGCCATTATTGAGTATTCTTGCTTTGAT/C/CTGTACGTAAAGCATGTAAGACT ACAACATTACGACCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAAAACATTTTGTCAATTAGAT T
WI-14510	104 A T	TGGCAAAATA TGCATAACAA AA	TTGAAAATGGT TAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTAGTGAAGTACACCCAGATATTTTGGGGAGAAGAG TTGTTTGCCTTTTGTGGCAAAATATGCATAACAAAATATTTGGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57 T C	CATTGGCAAT AAACACCATC A	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTGCAATAAACACCATCATTT/C/CTGCTGAG TCCACAGATAAGGTCCCGGAGAGGGGCTTCCCTCTCTCTCGCTGGTGGCTTCCCTCCACTCCAGCGAGT GAAGCCTTTTCTGGAATG
WI-12634	52 T C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTAT/C/CTGCTATTAGCTA TGTTTACAATTTGTCTGAAGGGGTCTAGATGTGTACACCCAGAAAGTGGTGAATTCCTGA
WI-15249	34 T C	GGGCTTGACAC AAAGTTCTAA AA	GGAAAGCCAG AGATTTTAAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTT/C/CTGTAAAAATCTCTGGCTTTCTGCTGGTGG TGAGGAGGCACAGGCTGGGGTCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCCTCCACTCCCGAG CCACATCTTGGCTCT
WI-12159	28 C T	AAGACACCGT GCAAAATGC	CCCTCTCCTCA GTGCACITTT	CTGTCCGGGGAAGACACCCGTGCAAAATGC/C/TAAGTGCCTGAGGAGGGGAGGTCTGTGACTC CCAAACCTCGAATATTTATGAATCTAAGAGTCCAGACGACGAGTTTCATCCACGGAGATCTGC
WI-12648	41 A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAATGCTAGTGGCATTAAAGATGCJA/GJTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACCTACTCCATGTTAGGTGCTTTACTTGGATTATCTCAGTTAAAAACCCACA
WI-12684	64 G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC/G/ TCCATTTAGGCTTTGTTTCCATTTAGAGAGCACAGGAGGAAATTTAGCATAATTTCTT
WI-15260	75 G A	AAAGGATGAA GCTAATCATG GA	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTGACACAGCGGACACTGTCTAAGTGAACAAAGGATGAAGCT AATCATGGA/GA/GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGAAATTA TCCCTG
WI-15325	39 T C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTGA	AAGTTTAAATGGACTCACAGTTCCATGTGGCTGGAGGCT/C/CTCACATCATGGTGGAAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123 C T	AGTTGGCATT AATAGCCTAT C	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTTATCCATGGCGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCCAGAACCTATGACCTGTATCTTCAGTTGGCATTCATAGCCTATC/C/TAACCTCCATGT GGGAGTTTCATAATAA

WI-14528	62 T	T T T T A A C T T T T T C T G G A T G G T A T A A A T	C T C G A T T A G C A C T T A T T A T A A A A A T T A A A	T A T G C T T T A T T G A A G A G A A A T A G G C T A T T A A T A T A T T T T A A C T T T T C T G G A T G G T A T A A A T T / G J T T G A A T T A T A A A T T T A T T T T A T A A T A A G T G C T A A T C G A G A C A T C A C T G G G T A T A A T T G A T A T T C T T T C G G T T C G G A T G C A A A C A A A A A A T T T T A A A A G A A A A T G T G A C T T C A A A G G A A A A G A A C A A A T T T C / J C A A A G A C T T G G G G A G T G A A G G C A G A G C C T G G T G C A G A T G G A C G A G G T C T G C A G A C G
WI-15347	74 C T	A A T T T G A C T T C A A A G G A A A A G A A C A	A G T C T T T G T C A C T C C C C C A A G T C T T T G	G T A T T T C T G A T G C T T T G A C A T C T G G G G C A T T G C T G T C T A G A G A G A C T A C T T C T C T G G G A C C A G C C A A T T T C T A G T G A T A G T A G A G G A C T C A / C / J C T G C A C G T G C A C C T T T C A T A T A C A G A T C A T T A T T G G C T G T C T C T G T A T A C A A T G T G T G A A A A C / G / A / J C T T A A T T C A G G A C A T C T T C C A C C T T G T T T G G C T T C C A G T T G T A C T G C A A G A C C A G T G T C A G G C A C A T A G G C T G A T T A A T C A G T G G
WI-14546	95 C A	T G A T A G T A G A G G A C T C A	A A G G T G C A C G T G C A G G	A G A A T T T T T C C T T T T T A A C A G G A C A A G T A A C A G A T T A C A T C A A A C T T C A G A A C T T C T C A A A T A C C T A G T T A T T A C A C A T T C C C A T C T G T T G C A / G / A / G G A G G A T C T T G G T C G G C T T A A C A C C A G C T G G A G T G G A T A A A T G C G G C A C C A C A G A A A A A C A C A C A G C T A C A C A G C C T G C A T T T G G C T T A / C / J G T G C T G A A A A A G A A G G G C C G A C C T C T T G A T A A A G A A T G T C T
WI-15353	37 G A	---	---	A A G T A G A C A C A A T A G A T G G C T C A A A A T A T C A G A A T G C A C T A C G C A C A T C A C G A G T A A A T A C T G T T T G G T A A A A C T T G T T C A G T T A A A T A T G T A / C / J G T G C C G T G C A T G T A T T A A T A T C C T T C T T A C C A G T C A C C C T A A A G A A C C A A A G C T T A G G A C T A G G A C A C A A C C A T G C A G A A A G A G C A G G G A G A C C A G A C A C T C T G G G T T G A G A T G A T T T T A A T G C C G C A G C C G A C A C C C A C A
WI-14580	100 G A	C A T T C C C A T C T G T C T T G C A	C C G A C C A A G A T C C C T C C	A A G T A G A C A C A A T A G A T G G C T C A A A A T A T C A G A A T G C A C T A C G C A C A T C A C G A G T A A A T A C T G T T T G G T A A A A C T T G T T C A G T T A A A T A T G T A / C / J G T G C C G T G C A T G T A T T A A T A T C C T T C T T A C C A G T C A C C C T A A A G A A C C A A A G C T T A G G A C T A G G A C A C A A C C A T G C A G A A A G A G C A G G G A G A C C A G A C A C T C T G G G T T G A G A T G A T T T T A A T G C C G C A G C C G A C A C C C A C A
WI-8540	73 T C	G G C T T G C A T T T G G C T T A	G C C T T C T T T T T C A G G C A C	A A G T A G A C A C A A T A G A T G G C T C A A A A T A T C A G A A T G C A C T A C G C A C A T C A C G A G T A A A T A C T G T T T G G T A A A A C T T G T T C A G T T / C / J A A A T A T G T A T G T G C C G T G C A T G A T T A A A T A T C C T T C T T A C C A G T C A C C C T A A A G A A C C A A A G C T T A G G A C T A G G A C A C A A C C A T G C A G A A A G A G C A G G G A G A C C A G A C A C T C T G G G T T G A G A T G A T T T T A A T G C C G C A G C C G A C A C C C A C A
WI-8039a	87 T C	---	---	A A G T A G A C A C A A T A G A T G G C T C A A A A T A T C A G A A T G C A C T A C G C A C A T C A C G A G T A A A T A C T G T T T G G T A A A A C T T G T T C A G T T / C / J A A A T A T G T A T G T G C C G T G C A T G A T T A A A T A T C C T T C T T A C C A G T C A C C C T A A A G A A C C A A A G C T T A G G A C T A G G A C A C A A C C A T G C A G A A A G A G C A G G G A G A C C A G A C A C T C T G G G T T G A G A T G A T T T T A A T G C C G C A G C C G A C A C C C A C A
WI-8044	107 C A	---	---	C A C A C A T T C A G A A G T T T T C T G C A T T G T C T T C T G A T G T C T A A A A G A T T T G A G C T T T G A C T A T A C G A T T T C C C A C A C T G A C G C A T T C A T A A G G T T T C C C C / C / A / J A T A T G A T T C T C T G A T T A A T A A G C C C G A A T T C T G G C T A A A G G C T T C C C A C A T T C A A G A C A T T T G A A G G T T T T C T C A G T G T G G A C T C T C T G G T T G C A C A A G A T G G A A C T C G G C T G A T G C T T C C C A C A C T
WI-8550	32 G A	G G G A C A T C A A T G C A A C A A G	T T T G T G G C T T G A G T T T A C A A A T T	C T T A C T A C A T G G G A C A T C A A T G C A C A A G T A / G / A A T T T G T A A A C T C A A G C C A C A A C T T A G T T A A T A A T C A T G G T A A G G G A C A T T G C C A A A G A G C A A C T G A T G C C T C A G T G A A
WI-8057	87 T A	---	---	T A T T A G A T A A A C C C T T T G T C C G A T T C A G G A T G T T A A T T T G C T C T T T A A A C T C T G T G A C T T T T C C T G G T C A A A A G G A C A G T / A / J A T G G A C A G C A G A G A G T G G G G T C T G A A A A T G A A T C T T T G T G T C A A G G C A C T C T G T G C C T C A C A A C T G C C C C C T G T C A G A G G A T G C T G C C T T C C A G C C C T A A A G A C A C T A G G C C T T T C A A T G G A C G G G G T T G A A G C A G C C A G A T G T A A G G

WI-6375	28 A G A A	GGTTATTGCA TATGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTATTGCATATGGAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAGGCACATATGAAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTTAACTGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATATAATCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTTATTATAGTTACTTAA CAGCTAAATAATAAGGGTGTTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]TATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T G C T G	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGTTGATA	TCCTTAGCCCTATTAGGCTACACTGTAGTCACTTCTATGAGAGCAAGGGAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCCTGGTAGTTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAAGTGGACCTTCAACAACACACGACGCTAAACTCTGAGAGAAAA[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAATAATTACATGGCCCTATTTATTAGGACATTTGTGTAATGTTCCACTTTGTTTAA [C/T]AATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAATAATTACATGGCCCTATTTATTAGGACATTTGCTGTAATGTTTCCACTTTGTTTT AAACAATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558a	42 G C ---		---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTCATA[T/C]AGGAATGGATGCTGTGTCAGAACATACTGCCAATAAATCTTTAAGAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCAGAGGGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAC
WI-6629	75 T C G T C A T A	TCCTTTTCAGAG AATAAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTCTCTTGCTTT TTACTTAGCAAGGAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCACTTCTCAAGCACAT T/CJACCCAACTTGAAGGTGATTGAACCCAAAATAATGGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGGGCCAAAGCTATCTGGTTATATTTGATGTTGCCAT
WI-6644	134 T C ---		---	TGCTAAACACCACTTATTAAAGGAGAGTACTAGGAAAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGCACAGACTCTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTAGCAATATAGCTGGTCTGTGTATTAACCAAGAGCGGTATCTGG
WI-6690b	106 C T A G C C A C A G C	CAGACTCTGG	TAGCC	

WI-6690a	28 T C A G A G	AAACACCACC ATTATTAAGG	GCCTGTGTTGG TAGTTTTTCCT	TGCTAAACACCACCATTTATTAGGAGAGT/CJACTAGGAAAACTACCAACACAGCATGTGAAAC AGTTGGGCACGGTGTAAAGGGCAGACACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTAGCAAAATATAGCTGCTGTGTATACCAAGAGAGCGGTATCTGG
WI-6770	53 A G A C A T C A C A	CAACCCCAA AACATCACA	GCCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAACATCACA/GJAATTATTTCAT ACTATTATACACTCCAAAAGCAAAATACITCACTGCAATCC ATTCTGTAGGCAAGGTTACGCAAAATCAGCTAGCACTAATCTTGACCAATGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTAGATGAATTTACATTTAAAACATGGTAACTCCAAGCATTCT TCCAAAACAAAGAA/TJAACATTTGGAATAGTCACITTAAGGAC
WI-6686	151 A G A	GATCTAACAG CTGCAGAATG	AAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAATGG/CJA/CTTCTCCTCCAGCTTTTGTGAACAAAAC AATCTCCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTTCCAGGTACAAAGGTCTC TAAATACTGCCAACTAGCATTACGTCCACTCTTGCAATCAATTAACAAAGGGTATTTCTCTCTTG GTATTTTCAATGATGCATTATACAAATAACGAAGTTAGAACTTAAATGCACCTGATTAATTATG TAACTGGTAATTTGTTTTAAAAGCATAAATTTGGTTCTTCTTCAATAAATGGAATTTAAA TATTTCTCTGATAGTCTTGAGGTT/CJATCATTATGATGAGTGCACAAAGTGTG
WI-6844	225 T C ---	---	---	CGGTTTGTACACTTAATGGGTTTTTTTTAAGGGATTTTTTTCAGGTCTTGTCAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAA/JG/CACCTTAGAAAAATTACAT GACACGGAGAAATGCGCCTTGTCTCTTGAAGAGCTTACAGTCTAGGGATTTGACAACTCACAGT CTTAGGAACCTGGCAAGTAAGGCAATTTCTTATCCCTAGAGCTATTGTG
WI-6824	112 A G ---	---	---	GTACAAAAAAGCTGAGAAGAGGCCAACATGGAAGTGTCAAGAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAAAGGAGTTAGATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTCT/CJAGAATAATTAAAAGCCACAAAGTGAACCTGTTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6889	139 T C A A T T C	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTTAATTAT TCT	TCCCAGCTCATATTTATTGGGCACAGAGTGGGCACCTCAATATCTGATGAACCTGATGAACGTAA AAGAGGTCTCCTTAACAAGATATCATCTCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTGGCTTCCCAAGGAATGTTTCTAATTTGGTTTCAAGCACACTGGTTC CACTTTTACCACCTT/CJCATGACATTGGACAATAGTACTACTCTTTCTAC
WI-6911	216 T C ---	---	---	GCCAGTCTCTAGTAAGTCTTAGGGACATGACCAGACCCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACCTTGGTGGAGGGATACCGCTGCTATCCAGATG/JAAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCATAAACAGAGGTATGA
WI-9413	112 G C ---	---	---	AAAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCCCAGCT ACAGCCTC/TGGTGATCTTAACCCCTCTCCTTT
WI-9557	74 C T ---	---	---	

WI-9617	37 G T	---	---	TGCTCTTTTATTTACAGTTTCAACAACACACGCCGCTG/TJGGCACAGTCTACCAAGTGCCCGCAG CGCCACGCTGGCCGGAAGTCTCATCTGTTCTGCTCTATGGACTGATTGAATTTGGGATGGCCAG CTOCAGAATGTTCCACGTGGGGCACTCTGTGGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGGTTGCACGATGCAGCTTGCAGTGGGTCCAAGCCGGGTGCTGTG
WI-9657	121 T G	---	---	AATGCTGGAGAAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAGT/GJATAATTCCTT TGTAATAAATAAATGTTTATAAATGTTTATGAAGCTCATACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114 G C	CCTCCCAAGTA GCTGGGA	AAAAATTAAC CAGGTGTGGTG T	CAGGTCCTGCTCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTG/CJACACCACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAAC
WI-13119a	51 C G	---	---	CAGGTCCTGCTCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTTC/GJACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAA C
WI-13112	71 C T	TCATAAAGAC TACAGACTTA AGCTTTT	TTAGAAATTTT GTGTATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTTG/CJCTTTTCCATATAATACACAAAAATTTCTAAATATCCTTAAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-12988	36 C A	CTCAGTACAA CTCAGTACAA	CAAAGTGTA CTACTGATGCT GTTT	TGTTAACATTTTATTGGTACGTGCTCTCAGTACA/CJAAACAGCATCAGTAGTGACACTTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAAAGTGTGTTGTGAGCACCATCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-13020a	108 G A	CTAATAGTGG AACCCTGAGA CTTT	CATTATTAAAC CCCTTTCAGA	TGCTATTTCATGACAGACACGCTGAGACAAATATCTTATTTACAGATGGAATAGACCCAGACATT TTCAGTACTTTAACCACTAATAGTGGAAACCTGAGACTTTA/GJATCTGCAAGGGGTTTAAAT GCAAATATCACATATATTTCCATTTTAAACACCATATTTAAGTTTCCATTTTCTTAAAGAAATGA TAAAAAATGTTTCCCAATAT
WI-12837	87 A G	CCATATACAT ATATCAAGGT AAAGTCCA	GCCATAGGAA ATGCTGTTTT	TGTATAAAAAATCCAACCTGTCCCAAGTACATATGCTCTATGATTTTATGCATATCATATATAC ATATATCAAGGTAAAGTCCA/GJTACAAAAAACAGCATTTCCCTATGGCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCAGGATGAGGCAGAGCA AGTGTGTCCA

L42611b	50 GC ---			GTGCTCAGGCCCTTCTGGCTGCAGAGCGCTTCTCAGGTTGCCTGTGCTCCTGGCCTCTAG TCTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTCCCTCAGCTTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTACATCAATGATTTACCA CTGGAGCTTCACCTTTGTTAC
L42611	34 TC ---			GTGCTCAGGCCCTTCTGGCTGCAGAGCGCTTCTCAGGTTGCCTGTGCTCCTGGCCTCTAG TCTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTCCCTCAGCTTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTACATCAATGATTTACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179 CT A	TGAAGAAATG GCTGATACCA	ATGTGCATTT TCACTGCAG	TGAACGTGTGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCAATTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCTGTCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 CA ---			TGAACGTGTGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCTAGAAACAGTG GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCAATTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCTGTCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 GC A	GCAGATTGGA AGTGTAATA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTCAG AAATGTAAGTGTGCGCTCACTGTTCTTACCCACTTAATCTGCAATTTTGAACACTAGATTGAAT TCCCTTGCAAAACCTTGTCATCATGGATACCCGAGTTAAACCGTTAATTAAGAGACATTAACATGG CCTGGTG
WI-1231b	141 GA ---			TCCATGGTTGGTTGCTACTGACTTGTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTATTCCTCTCTTCAATTAATTTCTT TCAC[G/A]TTATTCCTCAGCCTGAACGCCCTTCTCCTGCTAGTGACATTTAAATCCACTTTAC ACATTCGGACC
WI-1231a	126 TC A	GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTGGTTGCTACTGACTTGTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTATTCCTCTCTTCAATTAATTTCTT CTTTCACGTTATTCCTCAGCCTGAACGCCCTTCTCCTGCTAGTGACATTTAAATCCACTTTACA CATTCGGACC
WI-472	114 GC ACAGAAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCAGCCC	GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTTTAATTTTATT TTTTTTCAGGCATATAGACATAGATATCCATTATACACAGAAAAAG[G/C]GGGCTGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG TTACTCTATTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTACTCTATTTTGTTC/CTAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATAGTCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAACCAAC ACTGCCCA
WI-533	29 T C A A C T	ATCACAGCAG AGTACCTTTCT	CTTCCAACCT CTACACAATCT T	AGCATCACAGCAGATACCTTTCTAACTT/CATAAGATTGTGTAGAGTTGGAAGGAGGACAGGA CTGTCTGTGGTATAATGACCTGTGTCCAGTTAATCCA
WI-601b	112 T A ---		---	TCAGTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAAGAGAGGTTTCACTGACTCTAACTGAGTACT/CAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGTGAGTACAGGAT
WI-601a	74 C T ---		---	TCAGTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGC/CTGAACAGAAAGAGGTTTCACTGACTCTAACTGAGTACTCAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGTGAGTACAGGAT
WI-863	107 A G C C T C A C C A	CTCCTTCACAA CCTCACC A	CTTCCCGTAA GCCAAGT	AACAAAAACAGACACCCCTGGCTTCTTCAACAGTCCACATGGGTGCCAAACATCCACACATTCCT ACATCTCCCACTGGCTGCCCTCTTCAACACCTCACCA/AG/ACTTGGCTTACCGGAAGCATAAA GCCAAGCATTTAGTCTTTAATGCAACATGGTCTGGTGCATAC
WI-919	36 G A C	ACTGCTTGTCTT GTTGATTTAAT	TTATCTAATC CCACATGACAG C	ACTCACTGCTTGTCTTGTGATTTAATCAACCTAGCC/G/AGCTGTCTATGTGGGATTAGAATAAATA AACACAAAAATGAAAAACACACGATTGCTAACAAAGCAGATTCTTTTTTCAAGGCCACACGTAAGAT AATAACTTCAA
WI-991	37 A T ---		---	TGCATTCAATTATGCAACAAATAAATCTTGTACAT/AT/CATTATTGTATTTCATTATCACAAAT TATGAGTGAGGGATGATTGTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAGCCGGGATTCGAATCCATCAACTTGAATCCAGAGAAAT GTTCTGCATCACTGTACACACTGACTCCTTTTCTCCTTTGAAAAACAAGGC
WI-1011	70 G C C C A	CAGTATCTGA AGTTTTGTCT	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTGCAGTGGATCTGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTGTCTCC A/G/C/JAGAAGTCAATTTGTAGGTCTCTGGCGTTTTTGTACGTTTCCATTTTCTCTAATACACTGC CGTCTAAGGGAGGCTTGCAGAGCATTTATCAGATGGCTGTTTGTGCTGCTTCTGTGACTGAAG TTTCAATGCAAGGTCCTCATGTTTACAGATCTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAA ATGAGAGTGGCTTGTCTCATGAAATTTGGACAGCATGTTCCAGAGAGGGAACAGCATGGAGAAGA AAAAATCATACTCTATCCACGTGCAGAACTGGCAATAGTTTTGT/AT/TTACTAAAAACACAAATGT TTAACTTGGGGTCCACAAACAGGATATGTTGGCAATGTTTCTGTGATG
WI-5381	178 A T ---		---	CTATGTATTCATCTAGCAAAAGCAAGACTATTGGATAAGTTTCAAAAGATGAGAACAGGTCCTA GAACCTCAG/G/ATCGAAAGGAAGTTCATCTAGTCCATAGACCCCTATCTCACTGACCCCAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTTCCACCCCTGTTGT TAGGAA
WI-5791b	76 G A ---		---	

WI-5791a	44	C G ---			---	CTATGTATTCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTCGACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCATCTCACTGACCCCAAAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTTTGGCACCCCTGTTTGT TAGGAA
WI-5406c	120	C T ---			---	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C]TATGAGCCCCAC ACTTCTCAITTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAAAGAGAGAGGCAA GG
WI-5406b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT		CACCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAA[C]TATGAGCCCCAC ACTTCTCAITTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAAAGAGAGAGGCAA GG
WI-5406a	42	A G ---			---	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAG[A]G[G]GCCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCCCAC ACTTCTCAITTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAAAGAGAGGCAA GG
WI-5798	48	G C T G	TTTATTCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTTT TCAAT		CCATTCTCTCTCCCTCTCCCTTATCTCCCTGTTTCTTTTG[C]ATTGAAAAAATACTGGTT TTCTAACAGTGTCTGTATGGATACTATGTTATACATGCATAGTCTATATGGGTATCA
WI-5415	54	T A TTT	TCTTCATGAAT TCATCTTTCAG	GGACTAATTC A TGATCCGATCT		CCTGCTAATAATAATTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT[A]TAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T G	TCCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG		TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAGAG[C]TCTTAAACCATATTTTGTTT GAAACTCTGTGTCACCACTCTTGATGTGAGTGAC
WI-5481b	131	A G C T G C A G T C G	TGTCATTTATG CTGCAGTCG	TTACTTCCAGG CTCCAAGTATT		AAGCCAAITTCACATTAGTTGATGAATTTGAAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTCAAGAGGTAGTATATGTCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG[A]G/A ATACITGGAGCCTGGAAGTAAGACTTGGCTATTTTCACAATTA
WI-5481a	29	G A AATTT	CCAAITTCAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT		AAGCCAAITTCACATTAGTTGATGAATTTGAAATTTTACAGTATCTAATGCATGGGCATCTGTTTTC AACTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACITGGAGCCTGGAAGTAAGACTTGGCTATTTTCACAATTA
WI-5492	38	T C ---			---	TCATGAGTCTTCTTCAAAGATGCTTGTAAAGTCCCA[T]GCAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134 T C ---	CCCAATACITTT TTCAGGTGAA	---	TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTTCATGCTTCACATTTATTTTTT TTTCACITTAGTTAAATGCTTTTCCCTTGATCGTAGCAATGGCCAGTTTATACATATTTCTTTAGTC[C] TTCAAATTAATGCCACCATAGAAATAATTTCTAACCAACCAGCCAAACAGCCTCACTCTTCCCTT CCTGGTGCAITTACTCTTTACAC
WI-5546	40 C T A	GGCACCAGCCT TTTATAGAGT	CCTGTATTTTA GCAACATGGG	CCTTATAACCCCAATACITTTTCAGGTGAAAAAGGGAAAA[C]TACCCCATGTTTGCCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAATCTGATGTGGGAAATAT TAGAAAATTAAGCGAGAGAGGCA
WI-5552	97 C T	TTTATAGAGT	TGCACAAATTG OCCAGG	TGTTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACCAGCCTTTTAGAGTC[T]CCTGGGCAITTTTGCACACTAGTGTACAG
WI-5836b	161 C T ---	---	---	TAAGTTGATTTAAACACTCTGTGCCTCAATTTTCTCACCTATAAAAAAAGATAATAGTATCTAAAA AAAAGAGAGAGAAATTAAGGTGGATAGACATGAATAACTCTGATGATACTGTTGTATCCCTGAA TCTGCAATATACACATGATTCAATGAT[C]TCCATTTTGAAAAATTAAGCTTTTGAATTGTTTCCCA ATG
WI-5573	58 C T AGGTGGGA	GTTCATAAGG AGGTAAATGTG TC	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATCGTTCAACCTCGATGATGGCGTTTCATAAGGAGGTGGGA[C]TGACAC ATTACTCTCCAACGTTCATCAGAACACTTCAACAGCG
WI-5850b	134 G A ---	---	---	CAGGACCTTGGAGCCTTGTCTGTTTGTCTTCCACCCCTCACTCTTTCTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTATGACGCGCTCTATCTTCTATATGGGCAATATCCAATGTCCCATTG[C]A TTTTGGCCATTTCCGTATATCAAAACAGAGAAAGCAGAGGGTGG
WI-5850a	92 C T ---	---	---	CAGGACCTTGGAGCCTTGTCTGTTTGTCTTCCACCCCTCACTCTTTCTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTATGCA[C]TGCGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTG TTTTGCCATTTCCGTATATCAAAACAGAGAAAGCAGAGGGTGG
WI-5612b	125 A T TTC	CTATTAATGA GCATCGTGTCA TTC	TTCTCTTGAGA AACCTAAAAC ACTG	TGCCTGATTGACACATAGTTATCTGACAGTAATCATCTAACATCACAATAATCTTATTTCTGCCTG TCACACTAATTTGCAAGCAATCAATGATTGACTAATATGAGCATCGTGTCTATTGATTCAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTGTAACCTCAAGTA
WI-5612a	44 T A ---	---	---	TGCCTGATTGACACATAGTTATCTGACAGTAATCATCTTAACATTAACAAATATCTTATTTCTG CTGTACACTAATTTGCAAGCAATCAATGATTGACTAATATGAGCATCGTGTCTATTCAACAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTGTAACCTCAAGTA
WI-5636	26 A C CCGCAATAA	GCCAAITTTAT CCGCAATAA	CATCGAGGACT TTGGGA	TGAGAGCCAAITTTATCCGCAATAAA[A/C]TCCCAAAGTCTCGATGGAGGCATTTCAAGATCGGG GCAGGGGAGGCAGAGGTTGAGACAGATGTGAAGAAC

WI-5865c	103 C G ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTCTGACTCACTGCTGCTATCAAAAATTAAC/GJAAATATTAAATATTTTATTTACAGAGGAACTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAGGTCACAGTCTTCA GAGAAGACAGACAACTAAATAAATTCAGG
WI-5865b	99 T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTCTGACTCACTGCTGCTATCAAAAATTAACAAATTAATAATTTTATTTACAGAGGAACTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAGGTCACAGTCTTCA GAGAAGACAGACAACTAAATAAATTCAGG
WI-5865	165 T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTCTGACTCACTGCTGCTATCAAAAATTAACAAATTAATAATTTTATTTACAGAGGAACTCAGAAGCCAGAAAAATGACCAAGACACAGTJAJCCAGTCTCCATCTTCAAAGGTCACAGTCTTC AGAGAAGACAGACAACTAAATAAATTCAGG
WI-5874	76 T G ACAGAAAA	CATAGCATGG ATAATATTAT ATATGT	CCTAGTAAGTT TCAGTCATTG ATATGT	CTCAGACATTCATTTCATTAGTTGTTAAATTTTGTTATTTTCATAGCATGGATAATATTACAGAA AAAAAATTT/GJTACATATCAAAATGACTGAAACTACTAGTAGCAATTTGTTTGCAATTTGCT CATGGAGCCGACGTTGAGCCTCAGTTTTTCATC/AJTTTTTCATAATTTACTCTCTTTCTGTC ACAATGTTCTGCTCTGTTTCAACTCTCATTGCTGATGGATGGTAGTCATAAAATATGGGTGATTC AGAAAAATAAGTAAATG
WI-5752	36 A T TTTTCCATC	CAGCCTCTCAG AGAGTAAATT ATGAAAAA	---	TTAGCAGAAACAACAAAAATGTCACACACTGCAGTAAAGAGTGTTCCTCGATAAAATACGJC CATTAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAAACGAAAGCCGAGTTTCGATTACACACA GTTGCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCACGAAA CATTGTTGAAAAACGAAAGCCACGTTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760b	61 C G ---	---	---	TTAGCAGAAACAACAAAAATGTCACACACTGCAGTAAAGAGTGTTCCTCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAAACGAAAGCCGAGTTTCGATTACACACAGTT GTCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGJAJTCCCACGAA ACATTGTTGAAAAACGAAAGCCACGTTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760	187 G A ---	---	---	AATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTGJAJTGCAAGTTAGAT CCCACCCTCACTATTGAGAAGCTAAAGTGAAGACTACTCACTTCTCAGTCTTCTCTGCTGCTG
WI-5944	52 A G GGAATCTTG	TTCTCACCATG AACTTGCA	GGGTGGGATCT AACTTGCA	GAGTTTAATGAATCCTGTTCCCTCTCTAAAAACCTCTGTTCCGCCAACTTCACATTTCAGCAGATATT CTTTCATGGGTTATTTTGCCCAAGTCATGAGGAGATGCATGTAATTTGATCATTTCAAGAGTGTGAG TAATGCTTGGTA/CJTTTGCTCTGTGCCGTATCTGCTCCATCAATCACTTATTTTCTTATTT GCTGAATGAAACGGTTATTACAG
WI-5967b	148 C T ---	---	---	

WI-5967	165 CT ---				GAGTTAATGAATCCTGTTCCCTCCTAAACCCCTCTGTTCCCCCAACTTCACATTACAGAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGATGTAATTTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGCTCTGTGCCGTATC/TJTGCTCCAATCACCATTCCACATTTATTTCTTATAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53 GC ---				GGTGAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGCACTGAGCCCATTTGAGGGA GCATTTGAACCAAAACCCAGCAGCTGCTGACATTTGACATTCAGCAAAACCTTGATTGACGGTGAC ACACCATGCTTGGAGGAAGGAATGAGG
WI-6141	80 TC AGGTACTT	CTTCTTAATTA AGCATCTACA	TGAAAACCCCA GAACAGTG		GACTCTGTCTCAAGAAAAAATAAATTGAATAATTAAAGCACTTCTTAATTAAGCAT CTACAAGGTACTTAT/CJCACTGTTCTGGGGTTTTCAATCCTCTTACCTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAACAGGATTTACATGCAGAGAAAAATAGGGGAGATAAAAATTTGTCTTTT CTC
WI-6450	45 TC GTGCACA	CCAATGACTT ATTCTATATCT	TTGTTTGAAT GTGTGTACTT CT		ATAGGACAGTTTTCTTCCAATGACTTATTTCTATATCTTGTACAT/GJAGAAGTACCACACATTTCA AACAAGAGCCAGGTATGCCAGGTGGGATTTTTCACGGTCATGTAATATGCATGTAAGACTA TTTTACTGGCCTTCTTTATGCATAAACCAAGGATTTGGTCTATTCACAAACATGTGTCAATACAG CAGTTGTCATGTCCCTCTGTGTACTAGAAATATAGTCTTTATAGAATATGTGTTTGAATAAAGCCACA AATTATCTATAAAACAACA/CJJAAGGAACGAGGCTCAAAAGTGAACAAACGGCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAAAATATAATCCGTGACCTCTTA
WI-6461	88 CT ---				GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATTTCTGGTCACACAGGACTTTCTGGGCT ATGAAATAGTCTATTCAGTGAAGTATGATCATAAAAGACATGCAAAACCTTTTCACAGTCTTGT CCTGG/GAJAATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCTTT
WI-7466c	141 GA TTGTCTGG	TTTTACAGTC TTGTCTGG	AGTCGCATGCC AATTTATAAT		GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATTTCTGGTCACACAGGACTTTCTGGGCT ATGAAATAGTCT/CJATTGAGTGAAGTATGATCATAAAAGACATGCAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTCTCTT
WI-7466b	80 TC GTC	GACTTCTGGG CTATGAAATA	TGCTCTTTATG ATACTAGTTC ACTGAA		TGCTTTTAAAAATAACAATGACCACCACTGACACCATAGTCTGTCTCCATTGCCACGTCTCTC AGTAGAATAAGACAGGACTTTGCTGGTGTCTATCTC/JATTCTCTTCAGAAAGACACTTGGCCCT CATAGGCATTCATAGATAATTGTTGAATGAATGTGCTTTTGTCATATTGATTCCTACATTTGATACA TTCTCAGGAGGAGACTTTGGCCTAT
WI-9814	104 CA ---				CCTCTAACAGAAAACTTGACTTCTCAACTCAAAATACCTTCTCTAATAATTT/JAGJGTAACCA AAATATTCCTTCAATAAATAATCTTTAATTAGAAGAGCAACAGTGTAGAGGTAGTACATTCA CCAC
WI-9720b	55 AG ---				

WI-9720a	47	A G ---	---	CCTCTAACAAAGAAACFTGACCTTCTCACTCAAAATACCCCTTCTCTG/JGJATAATTTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123	A T ---	---	CACGCTCTAAGGAGGATGGCTTATGAGATACCTTTGCAATGTGCTGCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTCAGATGAAGGCTCAGGGTGCT/JAGAGGATTAG TAAGATCTCTTTCTAAAGACAGAGAGATATTTACAAGAAGAACTCACCAGGGTTAGTTTGCAIT TAAGAAATTGCCAGTCTTTTGCTCTGCATCATCTTGAACATTAATCCACATG
WI-9748	74	C G ---	---	CCACTTCAGTAAATCAATTTGTAGCACATTTCTAAAGATTTCTAATTTTATATGTTTACCCCTT GTCATTG/JTCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTTCCTGGAAATCTTTCAGAAT TACAGTTATGATGCTCTTTTATATCCCCA
WI-9943	91	T C ---	---	TGAGGCTATGATTGAGATTTGTAGTGACTAATACTTATTAAAGCAATTTCAATGTTGTGGGCACTGTT CGTTGTGTTTATATCCATCTCTG/JATTTTAAATTTCTACTGAGCAGAAAAAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTAATATTGCAATTCACACCTTCTCTTTTGTCATTTAGGGA
WI-9891	39	T C ---	---	AGGGGCTTCACAGATCCGTCAGCTCAACACTGCTCTCTT/JAGTGAGCTGTGAACCCACCCAAAGAC GGCTGGTCATCAGTGTCATCTCTCTCTTTCCGGACAACTATCTTTAAAGAAAAAAGAGTGT CTTTGAATGATCCATTTATCCCCAAATAATCTTGTTTAAATAATCTTATTAGGCCAAATCCCAAT GTGCTGAAATATCTGCCAAGCATGTCATCTACACAAAAAGGATTGCAAA
WI-9897b	84	C T ---	---	CTCAGAAATTATCAGATCTCCCCAAATGTCATGATCTTGTCTCAACATCTATTTTCTCTCAAAC ATTTATCTAGCCTGT/JCAAGTCATCCAGTGAGGCTGTTTATCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGACCCACATTA
WI-9897a	83	A T ---	---	CTCAGAAATTATCAGATCTCCCCAAATGTCATGATCTTGTCTCAACATCTATTTTCTCTCAAAC ATTTATCTAGCCTGT/JCAAGTCATCCAGTGAGGCTGTTTATCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGACCCACATTA
WI-9935b	115	C A ---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTGACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGGTGCTTGAGCTGGCAGGGGAGTTTCAGACA/CJAGCCCAAGAAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9935a	42	C T ---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTGCA/CJACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGGTGCTTGAGCTGGCAGGGGAGTTTCAGACACAGCCCAAGAAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9983	146	C T ---	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGCCACAAATGTTAGGCTGCCCTCCCATTTCTCTTGCTTGA TTCCCCAAACCCAAAGGTTCTCACCCAATCTGATCAATGCTAGTGGTCACTGGCTGGTCAGGGTAA AGCATATGA/C/JAGACACAAAGACAAAGAGGTTAAAGTTGCTGCTCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACJAAAGTAAGGCTTCGAGGAGGAGGTGAGCAAAGG

WI-10019	139	A T A T C T	TGATGTAATGC TATGTAGCAA	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTTTGGTTTATTTATGTGTGCTATAAAATCAATGGTTCTA ACATTCAAATAGATCTTTTGGTCTCTGCTCAGATGCTTCAATGATGTAATGCTATGTAGCAAAAT CTA/TJCCCTAAGCACAGTAATCAAGGCCTTCTACCCCA
WI-10020b	122	T A T T T	GCGAGAAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAAATATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTTATGGCGAGAAAAGAAATCATGACTTTTJ/AJAAAAATACC AGACTAATGATTAAATAAAATTAACAGTCTAGGGTTCCGGAAAGTGGCCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10020a	39	T C A T A A A T T	TGTCATCTTGA CTCGTATTAA	AAATTCCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAAATJ/CJGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTTATGGCGAGAAAAGAAATCATGACTTTTAAAAATACC AGACTAATGATTAAATAAAATTAACAGTCTAGGGTTCCGGAAAGTGGCCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10084b	170	C T T T T A C A T G	CCTTAGATAT ATTGTGATTGT	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCCTATGCACCAGATATTGTGGTGACACTCTGTTTAAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG[C/J]GAAATCTGGCTTCAGAAAAGTTAGGTGTT T
WI-10084a	54	C A C A G G G A A G G	GTAGCAGGAT CAGGGAAGG	CAAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGC[C/A]ATTATAATA AATAATAATTTGCAGAGCATCTCTCTCCTATGCACCAGATATTGTGGTGACACTCTGTTTAAATCCAGTAT TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAAGTTAGGTGTT T
WI-10289	29	T C C A A A C T C T T	TCTCTGTCCC CAAACTCTT	ATTCTTGTTGT ATTGAATGBAA TTAA	CCAGGGATTCTCCTGTCCCCTAAAGTCTTATJ/CJTTAATCCATTCAATACAAGAATTTATAGAA TATGCACCACATGCCACAAAGACACCCCTTATATTAGT
WI-1319	40	A T A T T C T T T	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCCTTTJATJACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTAGGTCCTGTTTATAATTTGGTATCTTTTGGCACAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTAACATTAACTGGTGCAGATGTTTAAACTTGTGAACCTGCAGC
WI-10316	104	T C C T C T T	CTGTTGATTT CTACCTCTATT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGGTGACAACTTAGTGAGGTGTAATCAGAAGCATCTATATTATTCACAGTCACCAACCTG GACTATAGTCTGTTGATTCTACCTCTATTCTCTTATJ/CJTAACCTTTTGGATACATTCCCAAAGCAT CATGGTCACTTCCAGTTATGAAAAGGATGTTTAAAGCCAGCC
WI-2572	61	C T T	---	---	AGTGAGTTGTGCACAATTTTGAGACATTCTGTGACCCCAACTTAAACACTTCTCCCACACJCTJAC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

WI-10368	31 C T	TGAAGCAACC AGGCTCTGTT	CAAGATAATTAT ATTTATTCTCT AAGAGGGG	GAGGAAGCTGCCTGAAGCAACAGGCTTGTTCCTACCCCTCTTAGAGAAATAATAATATCTT GAGATAGGGAGGAGCAGCCTGAGGACAGTCTGGGTTTGTCTACCCACTGGAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCCTGATGGATTGCCCTTCAGGG T
WI-10391	32 A G	CTGCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAAGTT GA	CCTCCGGTCTCTGCTCAGGTATGACTCCCA/GTCAACTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTCCAGGGGACGCTGACACAGCCTTTGCTTGTGTGACAAACAGAAATTCGAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCTTCTAATA GCAA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGCTGACTTAGCGGGTCTCAATAAATATTATCTTTTCATATT TTCCAATTATTAATACTAGAAATTTTACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTTT CTAATAGCAA/AC/AGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	GGTGCTCAAT AAATATTATT CTTT	AAATTTCTGTT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCTGCTGACTTAGCGGGTCTCAATAAATATTATCTTTTCATATT TTCCAATTATTAATACTAGAAATTTTACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	CAAACTCAA ATTGCTTTAAG TACTTTA	AAATCCAACA GTCAAGGCTTT C	CGTTGGGAATTTTCTATCTACCTAAATATGCGGTGATTAAATAATACATTTTAAACAACTTCAAA TTGCTTTAAGTACTTTA/C/G/GAAGACCTTGACTGTGGATTTTGTGATTTTCTTTTATTTCTTAATA AAACATGCATATTAAAGTTGTCAGCAAGATGACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	GGAATATTTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATTTTCTATCTACCTAAATATGCGGTGATTAAATAATACATTTTAAACAACTTCA AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGTGATTTTCTTTTATTTCTTAATA AAACATGCATATTAAAGTTGTCAGCAAGATGACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	CACAAATGTA ACAAGAAATTG ATCC	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCAATTTCCCTCAAAACCAGCTTAAATCACAATCACTTTTCTTCTGTA GAGCTCAAACTCAGTCTGAATGAAATTTGCTGCACAAATGTAACAAGAAATGATCCTATTC/ACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACAAAAAGTTTCCCAAGTGAATTTAGCCAAAATGAGA/C/TAAT TTGTTAAAAAAACCCTCAATGAAAGAGACAAATATAGTTCAAGATTCAAGTTCAATATTGT ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTCTTTCTTTTCTTTTGTG/CTCTTA GAATCCATTTGCTTTTGGCAGCATTCCTCTCCCATATTTTAAAGGAGAAATTCACCTTTTCT CTGTTGGATGATCAGGTTCTGCTCTCCCAATCCAGGAGGAGTACTATTACCCCATGGGGTCAT AGAGAGGATTAAACAGGGTGTGCTGCAATGGGAATTTTGAAACC
WI-10656	59 T G	---	---	---

WI-11169b	154 T G T T T T	TTAACCAAGA G T T T T C A T T C	CTAACTTAAAA A T C C T C A T T C A	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAATTTAAGCCTAAAGTAGTGCCTTTTAACCAAGAGTTTTTCATTCTTTTT TTTAAAAAAGAGCAGACAGAT/GJTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95 A G T T G A A A A A	AATAAGTGAA A G T A A C T G A C	AACTCTTGGT T A A A A A G C A C	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAATTTAAGCCT/GJAAGTAGTGCCTTTTAACCAAGAGTTTTTCATTCTTT TTTTTTAAAAAAGAGCAGACATTTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G ---		---	CAAGTCTTGGACCTTGGATAGGTG/JACCGGCTGAAGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTATATAGATCTTGTTCCTTTTGGGTTTACCCTAGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATCCAAAATAGCCATGGGTTTGGACAAAATAC AAGTTAGTGTCTCTAATTAATGGGCATA
WI-10686	133 C T A A G G	TGCCCTGTGC A A G G	CAATCTTAAA T T C A T G T G T A G A C A C A	AATAACCTGTGGCACATAAGGCAAACTACTGAGCCCAATACAGAGTGTTTTATGTTAATATTGAAA AAAGTCAAGAGAACAAAGATAGTATGTTCTGTAGTAATCTTGAATCTGATGCCCTGTCCAAAGG C/TTGTGTCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAGGG
WI-11175	77 T A A	AAATGATCTT T C T G C T C A A A G	CTGTTCTCACA T T C T T T T T G A A A A	GGTAGGATGATCTAGAAATGCCACTTTACAGCCACTGAAATATATGCTCCCAATGATCTTCTG CTCAAAGAGT/AJTTTTTTAAAGTTATCTACTTATTTATATCTGCTTTTTTCAAAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAAGTAAGAAAAAGAAAGCCAAAT TGGGC
WI-10694	144 A G T A T G A G T T T T C	TGCAATGCTT T G A T G A G T T T T C	GGCAATTTGTA A A G G A G G A A A	TAGAGAGGCTTTTCAGTTTCAGGTTGGAGGGTGGTGGAGTGAGATTCACCTTTAGAAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTTCTAAAGTTTCAAGTCTTTGCAAAATGCTTTA TGAGTTTTC/GJTTCCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGAAAGCTTTCT T
WI-2716	23 T C C	TGAATTCATCC A G A A A A A C A G	TCTCTTTTCTC T C T T G T T G T C A T T C	GTGAATTCATCCAGAAAAACAGCT/CJGAATGACAAACAAAGAGAGAAAAAGAGAAATAAGGTTTTGT ATACGACAAGTGGCTCAAGCAATTTTCTGTCTGCCAGTGCATGGAGCAGTG
WI-10719	115 T C G C C A T T C T A G	TGACTCTCAAG T G C C A T T C T A G	GCACTGCCAGC A G O C	CAGGCCCAACTCTGTCTAATAGTGTTTTGAACAGACACCTCAGTCACACAAGTTTCTTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCAGT/CJGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCCATAACTAA
WI-10721	40 A G C T T G C C A	TGGCTCTGCTA A G C T T G C C A	GAACTCCCAC A T A A A T A A A T C T C A	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCTGCTGCTTCCCTGCTTGGTTTGAAGAGTTGAA TCTGAAGATTCCCATGGTAAATAGTATTCCTCTCCCTGCTTGGTTTGAAGAGTTGAA

WI-11204b	88 T C ---			GCACGAAATTGATTATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAACTTTACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAAATAGTCTGAGGAAAAATTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA	TGATCACTTAA AATGTACATAA TACCTTT	GCACGAAATTGATTATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAACTTTT/AJCACTTTTATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAAATAGTCTGAGGAAAAATTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTCACT	GCTGTGCTTC CTGTATGTACA	AAGAACAATG CATAACAGAA CTTTAA	ACATGATTTCCTTTAGTGTGAGCTTCTTACCCCAAGAAATATCCCTGGTTTATGCTGTCTTC ATTGGTTCACCTC/AJTAAAGTTCTGTATGCAATTTGTTGAGTCCACATAGGTGTTAATCATCCCA CACCACCTGCTTTAAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGCTTTTCTTTGTACGAGTGTATTAAGAAATTACCACCTCTGTACATTTTGTAAAAAGATAGCACAG AGAGAAGCATTACAGGGCAGCAGCAACATGAGGTGTGTTTTCTGTATGTACAACTC/AJTCCAA CCATTAGGATTGTCACTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATTCACACATGGA ATAAGTCTA
WI-11215	68 C T ---			GAAAAAAGTTTTAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTCAGATTTATTTTAGT [C/T]ATTTTCTATAATATTTCTTGTAGTGATGGATTTCTATAAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTAACTTTTATCCAAAGCCCCCATTCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAAAA GAGACAAAAGAGATGAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18 G A ---			ATGAAAAATGCATTAGA[G/A]AATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136 G A GCGTGG	CATACCCTGCT AGTTGTGA		AGCCACAGTGGGAATCATTTACACTACCGAAATCAGCAATGCTAAAAATTGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCACTGTTGAACATTTGTTAAACATTTACCAGCATACCCTGCGGCTG G[G/A]TCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTACAGGCTACTGG AAAGCC

WI-11222a	25 C T A	G C A C A G T G G A A T C A T T T A C	T T T T A G C A T T T G C T G A T T T C G	A G C C A C A G T G G A A T C A T T T A C A C T A C T C G A A A T C A G C A A A T G C T A A A A T T G G G C T T T G G A T T T T T G T T T T G T T T T C C A T A G A C C C C A C C G T T G A A C T A T T G T T A A C A T T T A C C A G C A T A C C A C T G C G G C T G G G T C A C A A C T G G C T A C C A G G A A C C T G A C A G A C T C G T A A T G C T T T C A C A G G C T A C T G G A
WI-10775	39 C T	C A C T C	A T A T G A T G	T T G C A A G T T T G T T T A T G C C A T A T T A A T T A A T T A C A C T C T C T A C A T C A T A T T T C T T A G C A A A T A C A T C T A G A C A C C T G G C A C T C A G T A A G G A T A T T C C T G C A C G A A T A A T C A T T G T T A T C A T T A G A C A T T G C A G G A C C A C C A T A T G G A T A A A T G T T G T T A T A A G G C A A G C A A T T A T T G C A T G C A T T T A T A C G A A G G A A T T A A A T A T C T T C C T T A T A G T T G A A T T T A A G T A A A A A T A A A G T T A T A C A T A A T A C A A A A A G T T G T A G T A T A G T A A C A A A T G A A T T A G A A A A T T G C A G T G G T T G C T A G T A C A G G A A T C A A A T T T G G A C T A T G A A C A A C T A G T T G C T A G G A T T T C C A C A A A T T A T T T C A T G A
WI-11226	165 A C	---	---	C A G T G G C T G G C T A C T G A C A A A C G T A A C A T C G T G G C A G G T G G C A A G G G A G A C A T T T A C A G A G G T C C A T C T C T G A T G T C A C C A G C A G G C C A G G A A G G T T G A T C T G G A G T G G G A C A C A C T G C T C T A G A C C T C C C A G G T C C C T C A A A G G T G G G T G T A G A G G C C C T A C T G C C C T G C C T G G G G A C G A G A G G C A T C A G G C C T T A G T C C T C T G G G A C A G T G A A G G G C C A C C A C C A C A G A A A A T G C C T A G G T C T T G T A G C A A G A G A G A A A G C A T C T T C A T G G C A G G A A T T C T C A T T C T G T T T C T A G G G T T G T G G C T G G C C A T C A G T T C A A C T A G C C C T G T C C C T G A T C C A G C A C A C A T T T C G T A A C T A C C C T C T A G A A G T C A T G C A A A G A G A A A T G A T G A G G A C C A A C A G A A T T A C T T G G C A T T C A G G G T T T C T T A A A C T A T T T C T G C A G A A C A T T A G T A A A G T T T A A A T A A G G A T C A G G C T A C C A G G A A T A C A G T T A G G A A C A T G T G G A C A T A T T T C T T T A G T A G A G G A C T T C T A A A G G C T A A T A T T T G G A T A C A T T A G G C T C A T T A T G A A T C T C A A A A G G A G C A T G T A G T A G G C A T A T C T A A T A T G C C T T C C C A C G A G C C A T C C A C G T G C T C T T A G C A A A A A A T A G A A T A C A T C A T T C T G A A T G G G C A C A T T A A T C T G C A G G C T C T C G C T T C T A A G T C A C C T G C A G T T A G G T C T G C A G A C A C T G T G T A T A C C A T A T A A T C T G A T T T C T G A G C A G G A G G G A G G C A G A T G A G A A G G G C T G C T C C G T G A A A T A C T A G T T C G G
WI-10832	91 G C	A G G C T C T C C	A	G A T T T G A G T A T T A C A A A T T G C C C A A A G A C C A T T A A C A G A T T T A A T A G T T A A A G C C A A A C T A T A A A G A A T T A A C T G T T C A A A A G T G T T A A T C T C T T A A T A C C A A T T T A T A G G C C A C C A T T A A C T T C T G A A G A A A G G T C A G C A T A T G C A A C T A A A T T T C T A A A G T C C A G T T A G T A T T T C T G T G G T C C C T T A T C T A A A G C C T C T T G C A T C C C A A A T G T G T A A A T T A T T T A T T C T T G G T A T T T C G C T T A C C C A T A G T C A C C T G T C A A G T G T C C A G T T C C A C C C T
WI-10810	58 C T	G C A G G A A T	A T G	G G A C C A A C A G A A T T A C T T G G C A T T C A G G G T T T C T T A A A C T A T T T C T G C A G A A C A T T A G T A A A G T T T A A A T A A G G A T C A G G C T A C C A G G A A T A C A G T T A G G A A C A T G T G G A C A T A T T T C T T T A G T A G A G G A C T T C T A A A G G C T A A T A T T T G G A T A C A T T A G G C T C A T T A T G A A T C T C A A A A G G A G C A T G T A G T A G G C A T A T C T A A T A T G C C T T C C C A C G A G C C A T C C A C G T G C T C T T A G C A A A A A A T A G A A T A C A T C A T T C T G A A T G G G C A C A T T A A T C T G C A G G C T C T C G C T T C T A A G T C A C C T G C A G T T A G G T C T G C A G A C A C T G T G T A T A C C A T A T A A T C T G A T T T C T G A G C A G G A G G G A G G C A G A T G A G A A G G G C T G C T C C G T G A A A T A C T A G T T C G G
WI-10778	62 A G	A A C A T T T A C A	A G A T G G A C	T T G C A A G T T T G T T T A T G C C A T A T T A A T T A A T T A C A C T C T C T A C A T C A T A T T T C T T A G C A A A T A C A T C T A G A C A C C T G G C A C T C A G T A A G G A T A T T C C T G C A C G A A T A A T C A T T G T T A T C A T T A G A C A T T G C A G G A C C A C C A T A T G G A T A A A T G T T G T T A T A A G G C A A G C A A T T A T T G C A T G C A T T T A T A C G A A G G A A T T A A A T A T C T T C C T T A T A G T T G A A T T T A A G T A A A A A T A A A G T T A T A C A T A A T A C A A A A A G T T G T A G T A T A G T A A C A A A T G A A T T A G A A A A T T G C A G T G G T T G C T A G T A C A G G A A T C A A A T T T G G A C T A T G A A C A A C T A G T T G C T A G G A T T T C C A C A A A T T A T T T C A T G A
WI-10789	21 C T	G C T C T A G A C C	T G G G A	C A G T G G C T G G C T A C T G A C A A A C G T A A C A T C G T G G C A G G T G G C A A G G G A G A C A T T T A C A G A G G T C C A T C T C T G A T G T C A C C A G C A G G C C A G G A A G G T T G A T C T G G A G T G G G A C A C A C T G C T C T A G A C C T C C C A G G T C C C T C A A A G G T G G G T G T A G A G G C C C T A C T G C C C T G C C T G G G G A C G A G A G G C A T C A G G C C T T A G T C C T C T G G G A C A G T G A A G G G C C A C C A C C A C A G A A A A T G C C T A G G T C T T G T A G C A A G A G A G A A A G C A T C T T C A T G G C A G G A A T T C T C A T T C T G T T T C T A G G G T T G T G G C T G G C C A T C A G T T C A A C T A G C C C T G T C C C T G A T C C A G C A C A C A T T T C G T A A C T A C C C T C T A G A A G T C A T G C A A A G A G A A A T G A T G A G G A C C A A C A G A A T T A C T T G G C A T T C A G G G T T T C T T A A A C T A T T T C T G C A G A A C A T T A G T A A A G T T T A A A T A A G G A T C A G G C T A C C A G G A A T A C A G T T A G G A A C A T G T G G A C A T A T T T C T T T A G T A G A G G A C T T C T A A A G G C T A A T A T T T G G A T A C A T T A G G C T C A T T A T G A A T C T C A A A A G G A G C A T G T A G T A G G C A T A T C T A A T A T G C C T T C C C A C G A G C C A T C C A C G T G C T C T T A G C A A A A A A T A G A A T A C A T C A T T C T G A A T G G G C A C A T T A A T C T G C A G G C T C T C G C T T C T A A G T C A C C T G C A G T T A G G T C T G C A G A C A C T G T G T A T A C C A T A T A A T C T G A T T T C T G A G C A G G A G G G A G G C A G A T G A G A A G G G C T G C T C C G T G A A A T A C T A G T T C G G
WI-10828	23 T C	---	---	G G A C C A A C A G A A T T A C T T G G C A T T C A G G G T T T C T T A A A C T A T T T C T G C A G A A C A T T A G T A A A G T T T A A A T A A G G A T C A G G C T A C C A G G A A T A C A G T T A G G A A C A T G T G G A C A T A T T T C T T T A G T A G A G G A C T T C T A A A G G C T A A T A T T T G G A T A C A T T A G G C T C A T T A T G A A T C T C A A A A G G A G C A T G T A G T A G G C A T A T C T A A T A T G C C T T C C C A C G A G C C A T C C A C G T G C T C T T A G C A A A A A A T A G A A T A C A T C A T T C T G A A T G G G C A C A T T A A T C T G C A G G C T C T C G C T T C T A A G T C A C C T G C A G T T A G G T C T G C A G A C A C T G T G T A T A C C A T A T A A T C T G A T T T C T G A G C A G G A G G G A G G C A G A T G A G A A G G G C T G C T C C G T G A A A T A C T A G T T C G G
WI-10834	96 C T	G T G T T A A T	A G	G A T T T G A G T A T T A C A A A T T G C C C A A A G A C C A T T A A C A G A T T T A A T A G T T A A A G C C A A A C T A T A A A G A A T T A A C T G T T C A A A A G T G T T A A T C T C T T A A T A C C A A T T T A T A G G C C A C C A T T A A C T T C T G A A G A A A G G T C A G C A T A T G C A A C T A A A T T T C T A A A G T C C A G T G G A T G A T G T T C T G T G G T C C C T T A T C T A A A G C C T C T T G C A T C C C A A A T G T G T A A A T T A T T T A T T C T T G G T A T T T C G C T T A C C C A T A G T C A C C T G T C A A G T G T C A A G T T C C A C C C T
WI-2287	24 T C	---	---	T G G T A T T T C G C T T A C C C A T A G T C A C C T G T C A A G T G T C C A C C C T

WI-2296	81 A	GA	TGTTACTTTGA TTCCTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCTAGAAAGGTCTCAGGCTTTAGAATAAGTTGTTACTTTGA TTCCTTGCTCTGACAGCCAGTTAGCTGTGTGATTGCAGAAAGTTACATTTGTTTGTTG
WI-2300	77 GT	CCAGTCATAC	GGCACAGAAG	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCTCGAAATTTCTCTTTATTTGAGCGGGCAGGTGGTAGGCACAGAAGC CAGTCATACGTTTGCCTTAAATTTGACCCCAACCATTAAGAAATAGCATTCA
WI-2371	55 GT	CCAGCTTCT	GTCTTGTTCTT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAGGTCTGGTCTGTTCTTCCAGCTTCTGTTGTTGGTGGCT GTCAATCTTTGACATTCCTTGCTTGCAGCTGTATATTCATCTTGCCTCCAGCTTTACATGATGT TCTCTCCGTGTCTGTG
WI-2395	122 A	C TACTATCAA	GAACATATTT GTAGAAAAAT	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAATTTAGCTACAGTGCATATTAAGAGATAACATAGATATCATATAACTGGTTTAC TGAAATCTGAAACCTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTATCCAAAC/CJCTGAATTC AGAATAATAGAAAGGTGAATCATCTTATATCATTAAGAAAGCTAAATTAATTAGTAACAATCTTTA CAATTACAAAAACCCA
WI-2437c	192 GA	---	---	---	CACCAGCCACCACCTTACAACCTCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 GA	---	---	---	CACCAGCCACCACCTTACAACCTCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 GA	---	---	---	CACCAGCCACCACCTTACAACCTCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATG[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 GA	TTTATGTT	GCAACCTACT GACAAATTTAA	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCTTAGACCCCTCCAGAAATAATGCAACCTACTGACAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 TC	GAAAA	TGTTTAGGAA ATAATGACAA	TGTTTACAACCT GTACCAACAT G	CTGTAACCTACACACATCTCTCTGTAACTCTAGGTTACTTGTAAATACAAAACACAATGTAAATGCT ACATAAATAATTGTCATATATTGTTTAGGAAATATGACAGAAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAAGCCATTTTCCCCCAATATTTCAATCCACAGTTGTTTAAATCCACAG AAACCACGAATG
WI-2886	46 C/A	GGGAGAAGA	CAGAGTCTGG	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAAG[C/A]AACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCAGGCTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTGCAAGAAACAGAGGAGCGTT

WI-2906b	77 T A ---				CCTGAACACCTGGAGCACTTCCCTCCCTGGACACCTTCATCTCTGCTGGAACCTTGCCTGGAATGCTCTTCCCTCTT/A/GAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTACAGCTTCAAAGTGACCTCTTAGAGTTGGTTTCTGACCAACAAA
WI-2906a	50 A C TCTTCTGG	GACACCTTCAT	AGAGCATTCOA	GGCAAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTGGACACCTTCATCTCTGCTGG/A/CJACTTTGCCTGGAATGCTCTTCCCTCTGAGCTTGGCTTACTTTTCTTTTCTTTAGGTTTACAGCTTCAAAGTGACCTCTTAGAGTTGGTTTCTGACCAACAAA
WI-1736	175 C T ---				TACTCCTCATCTCCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCCCTAAATAGATTTCCACCCCCAGCACTATTTACACAGAAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGAGAAGCTTACTTAAGGACAGTGGTTTCCATCTGCTTCCCA/C/TJAGAGATCTAGGGTGTCTTTTGGAAACCACCTTGG
WI-1851	136 G A GTGTTAAGTA	GCATTGAATT	CACTAGCAATG	TTAAACTGAAG	AATACCCAGTCTTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTAATCTGGGAGGACACAAACATTTAGACCATAGCATTGAATTAECTATAGATGTGTTAAGTAATTAATAACATGGTACA/GA/JACAACCTTCAGTTAACATTGCTAGTGATTCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62 G A AGAGACCCC	CCCAAACAC	ATTGACTAAGA	CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTAGACACCCCAACACAGAGACCCCG/A/JTGAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGGCTGGTGCATAGTAGACACT
WI-1754	177 G A TAGTC	TTTTCTCCCTT	CTTAAAGAGA	AAAGTCGAATT	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTTTTCTCTTTCTGTTTGTCTTCTCCCTTCTTAAAGAGATAGTC/G/AJCCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37 T A TAGATTC	AAATTCAACC	ACAGATCTAT	TGTGATAGTTT	ACAACACAGCAAAATTCACACACAGATCTATTAGATTCT/AJACCCCATCTCAAAACTATCACATCAAGAGCAAGGAGACATATTACTGTGAGGAAGCCAAATTCAA
WI-3208	140 G A AGATAAAGA	GTGGAGTGGGC	TCACTCAAACT	AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGAGGTAGGGAAGGTGGGCAACTTGGCAGCAGAGAGGAGGGAAGAAAGTTCAAGACCGTTGGTAGGATAAGTGGATCAACCCCTTTGTAGGGCAGGTGGTGGAGTGGGCAGATAAAGA/GA/JCCAAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAG
WI-1775	47 C T TTTTCTCTG	CCTGCATGGTC	ATGACAATGAT	GTAAA	ACTCCACCACAGTTTTGTAGGCCAACCCCTGCATGGTCTTTTCTCTG/C/TJTTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A ACAT	AGCATATTCA	GAGGACTTAA	AAGGAGCATTT	CTGCCCCTTACATCCAAAGCCAGTTACTCGAGCATATTCAATTGATTTCCCTTACAT/GA/JCAAATGCTCTTTTTAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTTCCTTAGGA

WI-3416	33	C T G T C	CCAAGTTGTA GCATTGAGAA	AGGAGCAGAA CTACCTCTAAG AG	TCTGGTTCCTCCAAAGTTGTAGCATTGAGAGTCTCTCTTAGAGGTAGTTGTCTCGTCTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACTTCTCCAAACAAGTGTACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGTCTACCTCTGACGACACATAATTAATCCCATTTAAAGACCCAGG
WI-3453	70	C T A T C A G A G A A	TTC TAGGCC ATCAGAGAA	TCAATTTTCC CATGACTTC	TCCTATTCCTACAACAACAGAAATTTAACAAATTAATAATCAAGTGTGTCAACTGGTTTGA AATC/TGAAAGTCATGGGAAAAATGATGCCATGTGAATGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109	G A ---		---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTCCCTAATTTAGCACAGTATTTTATGAGGTGGTGAAGGAGAAAAATGATGGTTGCG TAGTTGAGTTTTCTGTCCACC
WI-3474a	90	A G A C	AGTCAGTTTCC CTAATTTTAGC	CAACCATCAAT TTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTCCCTAATTTAGCACAGTATTTTATGAGGTGGTGAAGGAGAAAAATGATGGTTGCG TAGTTGAGTTTTCTGTCCACC
WI-3502	79	C T G G A T G T C T	CCTGGGTTTCT GGATGTC	GGGTGACCTG TCTCA	TTTGACCCCATACATGAGATAAAACCATAAGAAATGGTGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTC/TCTGAGGACAGGGTCAACCCAC
WI-3600b	146	G C C A T C T	GGTTCTAAC TGGATATAA	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGAGTCTCTGACTCCTGCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/GGAGCCACCTAACTGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGG TAAACATCT/GC/TATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3600a	78	T G A T A G T T C T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGAGTCTCTGACTCCTGCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/GGAGCCACCTAACTGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3678	125	G T ---		---	TAAATCATGCTTATTTTTCACAAGGTAAATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACTTCTACTTACTGTGCTGTTATGATGCACCT/GT/CCTTTTGG ATAGATGGTTGATAGGAGATGGGTTTAAAGACACAATTTACCTTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTGTAATCACTGAATGAGTTCCAAAAGCCTTTATGTCTTAC
WI-3687	67	A C ---		---	AAAGCGATGTTGAGATACACATCCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T/A/CJAAAACTACTATAGTTTATGAAAAATGACTTCCAAAATTCAGAGAAAAGTCACTTAAACAGG ATTCTCAATTCAATCCAGAACTCTCTGTCAATTTTAACTTGTACTGCACAG
WI-3735	72	T C A A A A C	CCTCAGTTATG TATCAATGA	GGCTCACCAT CATTTT	TCTAAAATGTGAACCAAGAAATCCTGACAGCAGCTAACTGCCAGTCTCAGTTATGTATCAATGA AAAACT/CJACACCGGTTCAATGAAAAACAATGATTTGGTGAGCCATGTCCCTTATTTTAAATGAAAA GATCTTGGGCAATTAATCT

WI-1819	51	CT ---				GAAAAGCAGGAAGCCAGGACGACAACTTTTGAAGTCTTTTTCAGCAC[C/T]TCGTGGATCCG AATTTAGTGTGATTTGGCAGGCAATCGGGGTAAACATGTTCCAGTGTTTAACTTGCACAGAAATGC CAGATTAGCGATTGTTGACTTGTCCAAATTAATGAAATGTGAAAAAAGGGTGGTAACGTGT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGAATACG
WI-3746	116	GA ---				GGCCTATTCACATGACACTGGCCCAAGATCTTGCTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTG[C/G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	TC CAA	ACAGTCATTT AGTCTTCTCTGA	TAAGATAACC ATACTAGGTAG ATCCG		AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAAGTGAGAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCCCTTCTGCTATAG CATC
WI-3898	25	AC G	TGACCAATGTC TTTGAAGCA	TCGTGGTGTG CTCTOC		CAATGACCAATGTCTTTAGAAGCAG[C/G]GAGAGGACACCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCCACAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT
WI-3901	114	A G ---				GGACCATTTGCCCTCAGAAAGTACATTCAAGCCCTGGAGGCTGTCTTCAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAAACCTCGGCTTCTCCTCACCTGACAAGTGG[C/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99	CT GC	TGATCTTCTC AAGACTCACA			CTGAGGAGATTGATGCTACTTTACCTGAGGAACTTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATCTTCTCAAGACTCACAG[C/T]ACCATCCTTCTTGTCTTCTAGACCTATAACTAG ACTCAAGTCCAGCAGGCCCTTAAGGTAAAGTACAAAGTGTACCCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A A	CCAAGAGGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG		CCAGTCCAGGCCAAGAGCGTCTCTATGAATCAT[C/G]CATTTTGTCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAGGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	AT	TTGAGGTCTTA GTCATTGCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT		TAATTCACATTGCTCTTGTGTCATTTTGTGCTTCTTCTTATGTAACAAATCACCACACATTGAGG TCTTAGTCATTGCATG[C/T]GTATACAAATATGTCACTTAATAGGAACCTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTCTAATAT AGCC		TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCTTTTGGGTTAGGTGGCTTCTAAGATGGTAATT ATCTGTCCAAGTTTGTCTTCTAATTTAGCAACAATATCAACAGAA[C/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA		CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[C/G]TCTGAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACAGCAGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGCAGCAA ATCATGATG	ATGCCCTGGGATATACITTCACAAATGACTAGTATGAATAAGCAGGTATTAATTTACCTATTATATTT ATTCATCATGATTTGGCTGGCTTCTTTCCAAATTTACTACAAATTTGATTGTGCATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4189	51 A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGGCTGAACCACTCCCCAAGTTAGTCAATATAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAAAACAA TTCTGCTGTCACTGGTGGCTGTC[CTG]GGTCTGCTCTGTTCTTCAATGTTCAACTGCTTGTAT CTGTGCCCACTAAGGTATCAGGTTATATGGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTCTT GGAATTGCAACATTTGGGCAT
WI-5163	24 C T	CTGTCACTGGT CTGCTGT	AGGAACAGAC C	TAAGTGCATTAACTGTACAAAGTCCACAAATACCTTCCACCAAGTGCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAACAGGGGTGGGAAGGATCTGTAAAGG[A/G]TAAATATTGTTTT CCATAATTTGAAGATGTG
WI-4250b	117 A G	---	---	TAAGTGCATTAACTGTACAAAGTCCACAAATACCTTCCACCAAGTGCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAACAGG[G/T]GTGGGAAGGATCTGTAAAGGATAAATATTGTTTT CCATAATTTGAAGATGTG
WI-4250a	94 G T	TCAATATGAG TCTTGTGAAAC AGG	CTTTTACAGGA TOCTTCCAC	TAAATGTCTCGGGAGATAATAGAAAGGTCCCATCCCTCTGATACCTTGGTGTCTCCCCATCACCT [G/C]CCTTACACAACITGAAGTAGGCCCATCCAAACACTGGTCAGAAAGATAACTGTCTGAC ACAGCTCTTCAAATGGCACAATCAAAGCACCACAGTAAAGCAGAGGCAAAATCTGG[C/T]CTCAC CAITGGAAAAGTCTCTGAAGGATAAGGGAGTGAATGACTGCTAGAAGAGATGATTGGCCTT AGTTCACCTGCCTAGATGAGTAGACCATGTTGCTTTTAAATGACTCTTCTTCAAGATATCACAGCCAC GATG[C/T]TACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4325b	71 C T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGCTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C T	---	---	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCCCTGTCACTTCT CTAGACTCTTGACCTTGAGGAGGATCCCTGGCCTCTGAGTTTATCATCTCCCACTCCAGCCAG GGCCCTGTATCTGTTACAGGCC[A/G]GAATGCTACGGCTCACAACTGTGGGAGGTAGGAATGACGA G
WI-4347	158 A G	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGGCAAGTCTGTTGTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACAGTGGGACACCAGGGGTACTTGTATCACQ[C/T]CTCCCGCAACCCCA AGCAGCACAGCTTGACAGTCCAGGAAGACTCTTACTTCCACTTGAGAAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGGGA
WI-1936	117 T C	---	---	---

WI-5204	54	CT	---	---	TAGATTTTGATTGATGACAAATAGGGAAGCCCTTTGTTAAATTGGGTTTGAAGAA[C/T]GAAGAAAA TGAAGGGGAAGATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70	AG	CTCAAAA	TTGCG	TTTCCCTTATTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TATAGGCGAAACTATCTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112	TG	ATATAA	GTCTTT	CCCTGAAATGTGCTTTCCTCTCCCTCAACTCTCTAGGAACTTTTCCATGTCAGGTGAAGGTTTGA AGAGTACTTAAATTAACCTGTATCAAAAGAGATGGGTATATAAT/GJAAAGAACCATGTAAAGATTT CTTAAATTAGTGAATTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
WI-4456	49	CT	TATAGTTCC	GCATGAACTTG	ACACATTTCAATTTGCTTAAAGTTGAATATTACAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAGGTGGGGCAATTGATTGAATTGT
WI-4461	49	AG	CCTTCC	TTTGACCTTTC	CTGAACTAATGAGGTGCTAAATCACTGTTATTTTAAATATCTCTCC[A/G]TGAAATGGTGAAA GGTCAAGAAATGAATCCCACTTTTAGATTTCTGAAATTTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75	GA	---	---	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAAT TCACCTTTG[A/T]ATTTCTCTTCTACCTCAGGGAATC
WI-4465a	41	AG	ACACGAAAGT	TCCTT	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAAT CTTTCACCTTTTGTTATTTCTCTTCTACCTCAGGGAATC
WI-1949b	160	TCT	TAATC	GACAAAA	GGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT/GJCAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAATAA GGAGTGAATAAATGAATGCCATAATCT/CJCTGTGTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86	TG	ATGCTCTGAGT	GCCTTG	GGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT/GJCAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-4529	64	TCA	AAGATG	AAAA	TGAGAGATTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATTTCTGAAGATG[T/C] GAGTCTCTTTTATATCCTATGATTATTTTCAGGAAGTGTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGTGGTGGCAAGATGGGCCCTAGGATCATTTT

WI-4540	110 A G C A T C C	GCACATGTGG	GACAAATGCAGC CATGCA	AGCTTTCCCTTTTCTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCCAGTGCATGGCTGCATTGTCCAGTC AAATGAGACAACTTCCAT
WI-4582	226 T C ---		---	AGCAAGCATCTGGCAAGCCTGGTGACCAGAACATTAAATTCACCAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATTCCTGTACACA ATAACTTTATGGGAGACAGCATTGTAATCAATCAATAATGACTCGGTTGGCTGTACAAGCAT AAACAGACGCTTGCAAAATATGGTT/CJCCCTCCTTGTAGAAACCATTTGAT
WI-1965	105 G C A G	GCCATTGAGG AAGTGTTTAA	GAATGGATGGG TCATCTCTCT	CAAGGTTAGTTTAACTTGGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCCATTGAGGAAGTGTAAAG/CJAGAGAGATGACCCCATCCATTCCCTGG GCTCTTATATGACACCATACTATCCACACAGATGGGAGTCAATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99 C T T T G	CACTGTTTCT ATTGACCGTAC	AGAAAAAGAG AAGAAAGGAA AAA	TGTTAAAAACCATACAGTTTGTGCTGTACGTTGTAGACAACCCAGAAAAATTAACAGCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG/CJTCTTGTCTTTTTCCTTCTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38 G C C T A C G T T G T T	AGTTTGTGCTG	TTTTAATTTT TGGGGTTGCT	TGTTAAAAACCATACAGTTTGTGCTGTACGTTGTAAAGGAGTGTAAAGGAGTGTAAAGGAGC TACCAATTTTCACTGTTTCTATTGACCGTACTGCTTTTTCCTTCTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-4596	69 T A A G C A C T G T G A	TGAAGCAGAA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTGCTTGTGCTGAAGCAGAAAGCACTGTGA CT/AJCATTATTAGGCCATCTCCTGCCTGAAGCCTGCCTACAGCAATTTGTAAACATATGGCATGGG ACATATCTCTGAGCCCCAACAATAATTGACAAGATTCTCTTTTAAACA
WI-5252	119 A C ---		---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAGTCTTGGGAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAAATTAATACTGAATACTGTGTGAATCATTTGCTTTA/CJTACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G C T	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAAGGAAATGATAACCAAGGACTGTTGTTCAAGCAATGCTAGAAAAATATGCCTA/AJJC CAAGTAGACAACCTAAGCACCTAAGGCAAGTGAAGTTTCTCTTGTGCAATTAAGTCTCTATTCA ATTACCAATTTATCGGGTAATTAACACTGGAAGTAATGCCAGGCTAATGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77 C A G C A A A G A G G	GAGGCATGAA	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATCGGGGCAAAATTAAGCATATGAAAATACCAAGTGTGGCAGAGGCATG AAGCAAGAGG/CJCTTTTCATCTGCCCTGGTGGGTTTTCAGTAAGTCAACATGCTTTGGCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATTCACCTCCTAGGTATGCACCCTAAACATGGGTG GCAAAAT
WI-4649	50 C T T T C C G A A T G	GAGACCATTTCT	TGTACTAGGTG TACTTACAAGA AATCATC	TCACTGTTTAGAAAATTTCTTCTCCTCAGTGAGACCAATCTTTCCGAATG/CJTGATGATTTCTTGT AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGTCTACCTGAATTTGATTTTTTAA AAAATCCTCCCAATATG

WI-4650	148	A G G T C T T	GCACAAAGAA AGTATAAGTT	CTGAAGTGTTA AACTGGATTGG G	AACTGTGTGTATGTTGTTGTTGTTTCTGGAGAGTCAGTTACTCTCAGTATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCTAGAACACAAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT(A/G)CCAAATCCAGTTTAACACTTTCAGTAACGTT
WI-4677	82	T C A A A	TCCAAAAGTG ATTAGGTGAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTGAACATACGTGACATTTTGGAAAAAATTGTCCAAAAGTATTAGGTGAAAAAAT GAGTTGAAATAAATGTT(C/A)AGTTGAATAATGACACTGTTGAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGGAGACTAGAACACACAGCGTTTATAGGGGAATACTCAT
WI-4698	135	C G ---		---	ATGATGCTATCATGAGGAATCTGTAGAAAATTTTCCCTGGCAATGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTGACGGAAGAAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATCTG
WI-4722	88	G A A C A C C A C A C	TGCACATGG AACACACAC	AATATGGAATC TGCATTGAGTT G	CTTCCCATTTGCCCCAGTTAGATGACTGCTCTCCACCCAGCTAGAAAAAGATGGGAGATTTATTTTC TGCACATGGAACACACACAC(G/A)CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C A ---		---	GCCACAGTAAAGAGGAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACTTTGATGTTGAGATTTTCAAGAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGAT(C/A)CCAAAACAGCAGTGTGTCTAAAAAATATGATAGTTTCTTCTCCTGTCCACC GCAATGAAAAAGGAGTT
WI-2028	176	T C C T G T C T C A T C		GGTTGGAACCT CAAATTACCTA GAA	GACTACAGCCACAGACAGGCAATGTGTGGCTTGCACAGGTGTTGGTTTGTGTTTAAGTTAGATT TGAATCCTTTAAAGAAGAAAGTGGCTCTTCAAGTTTACTACAGACCTCATCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACTGTTTACGTTCCCTGTCTCATCT(C/T)CTAGGTAATTTGAGTTTCCAAACC TGTGG
WI-2033	183	T C A	GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTOC	ATGTGTATGAGCTCCACATTCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTCCAAGTTTATACAGGACCAGTGTGGAAATTTT AGCATTCTGGGTTTGGCATCCATCAGGGTGTAGAACTAATCCCTCA(T/C)GGAGAACGTGGAAACC ACTGATATACCAAT
WI-4745	131	T C ---		---	TTATGGATACATGTTTCTGGTGAAGGACAAGAGTTGAAGCAAAAGGACAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACCCAGGCCTCTCCACCAATTCCTCATCTTCTACTCTGA(T/C) AGGCAGACTTATATGGAAAAAGGGA
WI-2034	150	T C C A A G G A C	CCACAGTGCA CCAAGGAC	GGGTAAGAT AGAGTGCAGTT CC	CCACGACTATGCTTCCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCAAGA CCTCCTTCTGGGTTTCAAGTGAAGAACGATGAATCTCTTCACTCTCTACAGAGCTGGACTTCACCA CAGTGCACCAAGGAGT(C/G)GGACCTGCACCTATCTTTACCCCTTCCGACACCAAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	CT	TTAATTAG	GTGCTTTAAA GTGTGTAAGT	ATTTCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAAAAGTCACATTTCTCAATCACTCACCATTGTCTGTTATTGTCTCTTGCAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAAAAGTGTCTTTAAAGTGTGTAAGTATTA ATTAGATTCTATTGATA[C/T]TGATGTTCTTCAAGAGGAAATTTGTGTAAGAGGATTCCTCCATT TGCAATTCCTATGGC
WI-4782	113	CT	AATGC	GATCAGAAG ATAACTAGAA AATGC	GAACCTCTTG GTTATTTTCT GTTG	TCATTGACTTTTAGAGTCTCTTCAGTCTTTATGCTTATTCTTAGGAAAAAAGTGGCTAGGAGAA CACAATTGAGGTTCTCTCCAGATGCAGAGATAACTAGAAAAATGC[C/T]GAACAGAAAAAATAACCA GAAGAGTTCATTATGGTTTTTCCAGAACGATTAC
WI-4788	65	AG	TCC	GCATAGAATC ATCTTGCTAAG	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGACTCTTGGAACTTCAGTGCATAGAAATCATCTTGTAAAGTTC[C/AG] TTGAAAAAAAATATGCCCCAAATTTTAAATTTATCCAAACITTAAGTCGAGATTATAATTGATATTT AAAAAATATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	TC	CACTTCATTC	TCCAGAGAC TGATAATGGG GCTGTT	CTACTCTTCT ATTCATAATC CAAAA	CTTACTTCCAAAGTGTTCCTCCAGAGACCACTTCATTC[C/T]TTTGGATTATGAATAGAAAGAGT AGGTGTTATTATCTCTTTTACCAGGTGAAATGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGTCAGTGACAGAGCCA
WI-4818b	121	GT	GCCTGTT	TTGCCATAGAC TAGGTTATGTC	CCTTCTTTTA TATGTATGCCA GA	TATAATGTTTGTCCATAGTGGCATAGACTAGGTTATGTCCACACATGAATAACAATCTTATATA ATAATTTATCAAGAAAGGAAATATACATATGCGGTGATAATGGGCCCTGT[C/T]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	AG	GC		CATATGTATAT TTTCTTCTTG AATAAAT	TATAATGTTTGTCCATAGTGGCATAGACTAGGTTATGTCC[C/AG]CACAATGAATAACAATCTTAT ATAATAATTTATCAAGAAAGGAAATATACATATGGGTGATAATGGGCCCTGT[C/T]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	TC	GTAGCAGGT	TTCCATTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTGTTGATCTTTTGTCTGAGCCCTTAGATCTCTTTAAATTAATAGCAAGGTTAAT AATAATAATATGATGTTATATATACAATTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA[C/AG]GACTCATTTCTCTTTCATCTATTCTAGGTTATTGAGCCCGGAGATCTACCCAGG
WI-4888	56	GA	AAAGATAACA	GCAAGATATA AAGATTAAAGA	CAATCCACTA CCTCATTTAT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAGAAAAAGATAACAAG[C/AG]ATGAAT AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGTGCTT
WI-5328	44	AG	---		---	AACATTTTAAACCATGCTACATTTACAACACTGAAAAGACAG[C/AG]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACAGGTGATCTGGAAGAG
WI-4897	93	AG	---		---	GCCTTTTGAGTTTAAAGTCTTTTGGTGTCTTTTTCCTCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAAAGCGCTTGG[C/AG]GATAAACACATCTC
WI-5345	29	GA	---		---	CCCTGCTATAGGTCAGTTTAAAAATCT[C/AG]CTGCTATGTTGTTGTTGAGCCACATCCACT GAGGTATATTCTGCTGCATTTTCTATATCACTCAGCTTTCAGATCCACTCCACTCACTTGCAG

Accession	Position	Sequence	Accession	Position	Sequence
WI-5370	143 TCATAAAACAA	AATAAGATGG TACCTTAACCTA CAAAGTTGGTA CAGAGAATTC	WI-5370	143 TCATAAAACAA	ATAAACAATGCTTTGAAATTCCTGTACCAACTTGGCTTTTC
WI-9711b	423 TA---	---	WI-9711b	423 TA---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGAAACACAAAGAAACGCCTGGTGACAGGCC
WI-9711a	390 CA---	---	WI-9711a	390 CA---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGAAACACAAAGAAACGCCTGGTGACAGGCC
WI-9702c	345 GA---	---	WI-9702c	345 GA---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG
WI-9702b	344 CT---	---	WI-9702b	344 CT---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG
WI-9702a	179 CT---	---	WI-9702a	179 CT---	CTTTTATACTAGCTTTAAGAGGTTTTCATCCAGTGTCTACAGCATCTGATAG
TIGR-A003N21	49 CA---	---	TIGR-A003N21	49 CA---	TGATTACCTCTCAATCTATTGT
TIGR-A004V30	203 CT---	---	TIGR-A004V30	203 CT---	AAAGCGTCTTCTAGGTTAGTAGAAAAGTT

[illegible]

WI-7593	46 G A ---	---	---	TTTTGTTGCTCTGGACACCCACTGCTCCAGGATGAAAGGAGAG(G)AATGAGATCAGTTTTGGA CACTTCTCTTGAATATAAAGAAATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCCAA
WI-6962	78 A G ---	---	---	AGTGCATCTTGGGGAAAGGCTCCAGTGTATCTGACAGTTCCTTCAATTTTCAGGTGGACTCTT GATCCAGAGA(G)GACAAAGCTCCTCAGTGAGCTGGGTATATCCAGACAGAACCCAAAGTCTCC TGACTCTGGCTTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCACTTCACTTCCAC CTATTCTCTGAAATATTCCCTGAGAGAGAACAGAGATTTAGATAAGA
WI-7059	43 C G G C A T C	AAGCACCCA GGTCA	GCTCCTGCTG GGTCA	GCAGAGAAGAACCATGCCAGGGAGAGGACCCAGCCATC(G)GTGACCCAGCGAGGAGCCAA CTATCCAAATATACCTGGGTGAATATACCAAATTTCTGCATCTCCAGAGGAAAAAAGAAATAAA GATGAATTTGCAACTCTTAAAAAAA
WI-9063	53 A C T T	CACTTCACTGA AAGACACCAT	TCTACTTTCTG CCTTGGGT	AGCAGCCATCATGATCTGTTTTCCACTTCACTGAAAGACACCATTTAT(G)TACCCCAAGG CAGAAAGTAGAACTTACTATTCAATAATGTTTGACACAATTTGGAATTGTC
WI-7079	293 T G ---	---	---	AAGGGCATTGAGACTATAAGAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAATGCAT CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTTATTTCTTTCCATTGCT TATCTTGAGCACAAATGATAATCAATTTATACATTTATACATCACCTTTTGACTTTTCCAAAGCCC TTTTACAGCTCTTGGCATTTTCTGCTAGGCTGTGAGGTAACCTGGAT
WI-9074	38 A G A A A G	GGTAAAGTT CTTTTGCTCT	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAGTTCTTTTGTCTAAAGAA(G)AAGGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAAATGTAACTGT
WI-7104b	249 C T ---	---	---	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTTGACCACTACGTTGGGA GAAAGAGAGAGTGCCAGGAGACCTGAGGCGAGCCGCTTCTACTTTGGACTGAGAGAAGGAGCC CCAGGCTGGAGCAGCATGAGGCG(C)A/CAGCAAGAAGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GTGAGGCTTGACCAAGGTGGGGCCACAGCACCCAGCAGCATCTTTC(T)T
WI-7104	157 C A ---	---	---	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTTGACCACTACGTTGGGA GAAAGAGAGAGTGCCAGGAGACCTGAGGCGAGCCGCTTCTACTTTGGACTGAGAGAAGGAGCC CCAGGCTGGAGCAGCATGAGGCG(C)A/CAGCAAGAAGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTAGGCTTGACCAAGGTGGGGCCACAGCACCCAGCAGCATCTTTC(T)T
WI-8974	34 C T A A G A C T C A	CCTGAGCCCTC AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA(C)TGCCAGCTCAGCCCTACACCAAGTTTCCACC TGGAGTTTCATGCAAGGGCAAAAGGAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T C T G G C	CCTAAGCATTG CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTAGGGTGAGTTAGCATTAACCCCAACCTCATTTTAGTTGCTAAGCATTTGCCCTGGC(C)TTC CTGTCTAGTCTCTCTGTAAAGCCAAAGAAATGAACATTCCA
WI-9014c	93 T C ---	---	---	CCCTGTTCCCATGCTGACTGTGTTTCTCCCAAGTCACTTTCTGTTCCAGAGGTTGGGGCTGGAT GTCTCCATCTCTGCTCAACTTTAT(T)G(T)GCACTGAGCTGCAACTTCT

WI-9014b	44 C T ---		---	CCCTGTTCCCATGCTGACCTGTGTTTTCTCCTCCCAGTCATCTTTC/TJTGTTCCAGAGAGGTGGGGCTG GATGTCCATCTCTGTCTCAACTTATGTGCACCTGAGCTGCAACTCT
WI-7023b	206 C A ---		---	TCTGAGAGAAATGACTTGTGGGAGACACCCTGCAGATCCTCATGGGTTTGTGACAG[AC]CCCTCGGT CAGTGCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGGTCCCC TCTTTTGGCCCCAGATTTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAAACAC A/C/AJACACACATTCTTGCTCTACCCAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---		---	TCTGAGAGAAATGACTTGTGGGAGACACCCTGCAGATCCTCATGGGTTTGTGACAG[AC]CCCTCGGT GCTCAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGGT CCCTCTTTTGGCCCCAGATTTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTGCTCTACCCAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---		---	CTGAATCCCTCTCTGCCCTGGCTGGATCCGGGACCCCTTTGCCCTTCCCT/JTGCTCCAGGCC CTACAGACTTGTGTGACCTCAGCCAGTGTGCCACCTCTCTGGCCCTCAGTTTCCAGCTATG AAAACAGCTATCTCAAAAGTTGTGAAGCAGAAGAGAAAGCTGGAGGAAGGCCGTGGGGCCAAAT GGGAGAGCTCTTGTTATTATAATTGTTGCCGCTGTGTGTTGTTA
WI-9171	62 G A ---		---	ACATATCTGA AAAATGTTGAAAGCCCTAAGCCAGGAATAAAAGAAAAAGTAGAGATAATAATCA[G/A] TTCTTACAACCCGATGTAATTAAGCTGTGATTCAAGACTTCATGC
WI-9174	47 T C T		---	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCCTATTATTC/CAGTCCCTGTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGCGAGCTATGGTCAAATTGAG
WI-7753	52 A G GAAGAACAGA A		---	AAGGCCAGATGCACATCCCTGGAAAGGACATCCATGTTCCGAGAAGAACAGAT[A/G]ATCCCTGTATT TCAAGACCTCTGTGCACCTATTATTAACCTGCCCTGCCACAGAACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAATOCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A CGCA		---	AAAGAACTACAGAGACGATGTCCAAAACAAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCCGCA[G/A]ACCTAGTCAGACTTCCCTTTCATCTT
WI-9193	94 G A CA		---	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTTGACAGAGAATAA CTCAGAAATATTGTCTGCCCTTAAAGCA[G/A]TACCCCTCTACACACACACCCCTGTCCCTC
WI-9015	48 C T ---		---	TTTGATTGATATCGTGAATCCTCAGCCGAGAAATGGGGCTGGATTG[C/T]GCTTTGGTTAATACAT CTTTCCCTAAAGAAGATAAACACAAATCCATTCCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G AGGAGCCAC		---	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGCCAC[AC]VIGTCCCTAATGACACCCACTCTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAAGGAGGGAGCAGCCACTCTCTCAATGC TCAATGGCTCCCTGAATCAAGACAGG

WI-9231	32 GC	CAGTCCCCA GATTGA	CAC TTGCCAC ACTCAGAC	GTGACCTGTGAGGTCAGGTCCTCCCGAGATTGAGTCGTGAGTGCGGCAAGTGTGTCAAAGGGGGC TGCCCCCAGGAGATGAGGCTGAGAGCAGGAGTTGAGGCCGAAGTCA
WI-7836	120 TC	CAATAAACA ATGCAACGTTG	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTCAGTAGTTACTGAAAGAAAACTCTGCTA GAATGATAATGTATCATGGTGGTCTATAACTCCAAATAAACAATGCAACGTTCCCTTCGTTGATTTCTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACACGCT
WI-7286	65 TC	CAGCTTCAGCT TAACTGACAG	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCTTTTGGCCCTGCAGCATGTCTGCTCCCGAGAAATTCAGCTTCAGCTTAACCTGACAGATT/C TGTTAAAGCTTTCTGTTAGATTGTTTTCACCTGGTGATCATGTCTTTCCATGTGTACCTGTAAATTT TTTCATCATATCTCAAAGTAAAGTCA
WI-7858	91 TC	CTAAGCATGT ACGTGAATTTT GTAAAT	CCCAATTTTA TTAAAGTTTA CATCTAT	CAAAATCTTGGAAATATCTCAATGTAAATAACAATATGAATTTTCTCATGCATACCTACTATTACTACT AAGCATGTACGTGAATTTTAAATTTGTTATAGATGTAAACCTTTTAAATAAAATTTGGGGTGTGG
WI-7860	50 CG	A CG	---	GAAGATTAGGGAGGGTGTCTCTGTGGTCTCTCCCTGCCCTCTCCCA/C/A/GTGGGAGAGACC TGATTTGCCAAGTCCCTGGACCTGGACCACTACTGGGCTTATGGTTGGGGTGTAGGCAGG TGAGCGTAAGTGGGAGGAAATGGTAAGAAGTCTACTCCAAACCTAGGTCTCTATGTGACAGCCAG ACCTAGGTGCTTCTAGAGGGAACAGGGAGACCTGGGCTCTGTGGAT
WI-9084	29 AG	CGTACCTCCAA ACATAATTGA TTC	GCTTGAGTGTA AGTCTGCGAGA	CAAGGGGTACCTCCAAACATAATTGATTCTGAGTATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTAGGGAGGGCTGGCTACTGCTCTCTGCACTCTGCTGCTTG
WI-7307	128 GT	---	---	CACACTTGCTGTTCTTCTGAGTCTGAGTCTGCGAGGTGAGGTGAGGTGGGTAGCCGGGTTCCACA GGCCCCAGCCTGGCAGGGTCTGGCCCCCAGGTAGCGGAGAGCAGTCCCTCCCTCAGTG/TA/CT GGAGAGGGGACTCCAGGAATGGGGAATGTGACACCAACATCCTGAAGCCAGCTTGACACCTCCAGT TTGCACAGGGATTGTCTGGGCTGAGGGCCCTGTCCCAACCCCGGCC
WI-9274	25 CTG	GAAATGTGAC TTCACTTTGGT CTG	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACTTTTGGTGCTCAATGGACAGAAAAATTCCTGCTACATAGGAGAA GTTTGAATGCACCTAATAGCTGGTTTACACCTTGATTTCGAGGTGAAA
WI-7313e	266 TC	---	---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTGATTAGTAGGTCTGTGATTAAAGTTCTTAAAT TGTTTGACAGTCTTTATGTTTATTATCATAGGTATAGGTGAGCCTAAATTCCTTATCATATCTTTATT AATCAGCCAGTGTATCCACCAGTTTTTGTATTGTTTAACTAATCTATCTCTGATTTCATG AAGGTGAATATCGTTTTTGTAACTGAATAGAAATGTATAGCGATGA
WI-7313c	256 CT	---	---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTGATTAGTAGGTCTGTGATTAAAGTTCTTAAAT TGTTTGACAGTCTTTATGTTTATTATCATAGGTATAGGTGAGCCTAAATTCCTTATCATATCTTTATT AATCAGCCAGTGTATCCACCAGTTTTTGTATTGTTTAACTAATCTATCTCTGATTTCATG AAGGTGAATATCGTTTTTGTAACTGAATAGAAATGTATAGCGATGA

WI-9281	68	GA	---	---	ACTGTGGGAGACTGTGAGGATCCAGGATTCTGATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG [G/ATGTTAGTTGCGAGTCTGTGCTCTCCCTCTCTTATGACTGTGTCCC
WI-7848	142	A GCTC	---	CATTTATTTG AAAGCTATTCA GACA	TTCTGAAATATAACCCAGCCATTGAGCTATTTAAACCTTGTAATTTTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTCGTGACAAATAAACATTAAATGCTAACACATTTTTTAA ACCGTCTC[A/G]TGCTGAATAGCTTTCAAAATAAATGTGAATGGT
WI-9304	70	GA ACTGA	---	COCCACAGAAC TATTGTAAAC AA	TCACGTTGGTGCTTCTCAGATTCTGAGGAAATGCTTTGTATTGTATATACAAATGATCACCAGCT GA[G/A]AATATTGTTTTACAATAGTTCTGTGGGCTGTTTTTTTGT
WI-7933b	314	CA	---	---	TTACAGAACTTGCCTGTGCCTGTGTCCCTCATGCTAGGGCGGAGGGTCTTTTCTTCTTCTTTCC TACCTACCCCTTTCTTTGGCCAGGGCTCGTATCTACCTTTCTTTGTCCTGCTGGCTGGCTGCAC AGAGGATTGCCCTTCTTTTTCAGAGCTGGCCCTCGATGCCAAATAGCATTTAGTATTTTGCACAA AGTCTAAGGGACCATGGCTGCCTGGCTTGGGAGGAACCATAGCTCCCT
WI-7933	96	GC	---	---	TTACAGAACTTGCCTGTGCCTGTGTCCCTCATGCTAGGGCGGAGGGTCTTTTCTTCTTCTTTCC TACCTACCCCTTTCTTTGGCCAGGGCTCGTATCTACCTTTCTTTGTCCTGCTGGCTGGCTGCAC CACAGAGGATTGCCCTTCTTTTTCAGAGCTGGCCCTCGATGCCAAATAGCATTTAGTATTTTGCAC CAAAGTCTAAGGGACCATGGCTGCCTGGCTTGGGAGGAACCATAGCT
WI-7374	182	T A	---	---	CCAGATGTGCCCCATCAGCTTTTCTGAGGCTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATATTTGAAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTGAACCACTTTCTAGCTGCTTTGAAGAATATATTGT[A/C]AGAAACACACAAGGCTT GAT
WI-9343	78	C T CCTCTGCCA	---	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCTGCTACCTTGACCCCTTCCCTTCTCTGCTCTCTCTCTCATCATCTCCCAACAACAT CCTCTGCCA[C/T]ACACAACAACAAACGTAAGTTTCATTTGGGCAA
WI-7386b	104	T A	---	---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGTAATGTAACAATGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A G	---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTCACCTTTTGTATTAT GCTCTTA[A/G]TGATTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9360	79	T C TTGG	---	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAACTCG CTTTAACTTGG[T/C]ATTCCTCTAATGTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107	T C GTTCC	---	GGTCCAGAAGA G0003	TGTCCTCTGTCCTCATCTGAGTGGACCCAGGCAACCCCTTTGAGGAGTGGGGTGAACCTGCTCCTT GGCAGGGATTGTGACACTGCTGCTGGCTGTGTTCC[T/C]CGGGCTCTTCTGGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCTGGAGGGTGGTGAATAAAGGCATACTGTCT

WI-7424	131	T A A A A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGAAGAGCAGAGAAAGTTAGAGAAAAAGCCACCGAGGAAAGG AAAAAACATCGCCAACTAGAAACGTTTTTCATTCGTCATTCCAAAGAGAGAGAGGAAAGAAAA T/AJACAACCTTTCATTCCTTTGACAGGTTTCAAAACATTCCTACATA
X86400	118	A C			TCCTGCAAGAAGTTCTCAAGCCTTTTGGATTTTGTGCAATAAAGTACAGCTTTCATAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTTCTCTAATTTAAGTGAGA/CJCTCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTCAGAAATCTAAATTTATGTACCACCTCGTTTATTGTTTCATTCATCCA TCCCTTTTCCCATGAATATTCA
WI-8053	242	T A			GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGCTCTATGAATAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAAAAGTGTCCCATTAAGGGGACTTTTAAATCAACCTAA TAAACTCTAATTCGTGACTTTTAAAGATCTAAGGTCATTTTAAATACATGCTGAAAGGGTCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAAT/AJITCAGAAG
WI-6190	165	G A			TACAAATGAATTGCTTTTATTCGGTATGCATCCACATTTACAGCATTTAGTGTCTGAAACAGCAAG TGAAAGAGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTGGGGATCTGTGTGCACACCGG GTTCTTCTTAATCCCTGCTGAGGATCTTG/AJGAAGCAGCAGCAGCACCACCAAAACCAAGGCATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTCAGATTCCAAACTAGACOCOA
WI-6275	148	G C			AACAGTCAACCAACCAACATGACAACCTGCCAGGCAAGCCTTCTTCCCTCCCTTTCGCTGCC ATGTCCCTAGTCAAGGAGGTGCGGGAGGCACCGATGTTAGCTTCCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAA/G/CJGGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAACTG ATTTGCTTCAGTAACCTGGTATGCTGAA
WI-6421	41	G T			ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTGTG/JGGGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGGCTCTCTCACA GAATATTTGGGGCAGAACCCCTGGAACCTGGCCACAGGACATCCCAATATCCCTCCTCCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215	T A			GGGTGAGACGGGTTTATGTGCACATTTACACAGCTCAGCGTCTGGGCTGGCAGCGGCCATGCTC CTGTGGTCGGGCTGCTCTACAAGGGCGTTCACTTTTCTTCCACACACTATGTACAGTCAGTCTCCAA GGTGATGGGCTACAGTGTGTCATCAGTGAGTGTGTACACACATTTTACATAAATTACACACGACTC ATACATGAAAAAT/AJAGAGCCTAAGGGCCTGTATTTTATGAGAAAAAA
WI-9420	202	G A			AACTGTTTACAAAAAGGCTTTGCAAACTTCATTACTGAATTGTAAGTCAATGACTGTGTTGTTT TAAATATGTACCAAGGAAATACAAATTGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACGTGCACAAGGTGCAAGGAAACCGAAACCCATTGTGTACACTGTCTTCACACAG G/AJGCACTTTCTCACCTTAAGTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G A ---	---		TGGGGCTGCTTTTACACTTCATTTCTAGAGCAGAGCACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCTTGCCCATGGTGTAAACCTACATAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCO TTTTAAGAAAATGGCTTGGTTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCCTGCTGGCTTGGATTTATCCAAAGCGCATGTTCTTAACGTGCGCGTGAGCAG
WI-9470	204	G A ---	---		ATGTCAGAAGAGACACAGACAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCCAGGTTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCCAGATTCTACTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAGGGCTCACCTTCCCAAG
WI-1245b	201	G T ---	---		GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTCCTGATGAGATCTGCTGAGCCATGTCTGGCATCACAGGGTGGT TTATTAAATTTCAATTTATCATCTGGACAGCCCCCTTCTTAAACGTACATCCTTGCCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---		GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTCCTGATGAGATCTGCTGAGCCATGTCTGGCATCACAGGGGT GGTTTAAATTTCAATTTATCATCTGGACAGCCCCCTTCTTAAACGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---		TTCAGTGATAAGGACAGGTCTAGAACAAGCGTCCCAACCTGGCACCATAACAGTTGGACCAAA TAACTCTTTGTTTCAGGGGACTGCTCTACACATTGTGGGATGTTTAGAGCCTCCGCTGCTTACCCCA CTAGATGCCAGCA[G/A]CACAAACCCCTCCCCAACAAATCATGACAATGAAATGTCTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCACCTGGTT
WI-5385	110	G A ---	---		AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAAATGGTGGGATTGAAGAGG GAAGTCTCGATAATTTTAAACATATGGTTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCTCTGAC CCCTGCTACGGGAACATTGAATGCA
WI-5403	199	T G ---	---		ACCAAACCGTTGGCAAGGCTCCCCAAGACTCACCCACCTTGTGCTTACCCCTATGCCGGGTG GGATTGAAGAAATAACCAATAATATATTGCTACAATTTTCCAGTAGTTACCAAGGCCAGCCTAT TGGAAGAAATCATAAATGTAACCCCTACAATGTATTGCTCTGCTGGCTGGTCCAGGCATAGAGTT/G TGGCTACAACCCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A ---	---		TGGTATTTTCTCTTCTCTAAATGTTATGATTAATTTAGTGTCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]JAGGGAATGAGAAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGGAAGCCCAAGGAAAGTTAAGT

WI-5801a	48 A G ---	---	---	TGGTATTTTCCTTTCTCTAAATGTTATGATTAGTGTCTTTG/G/GAATTTGAAAAAATGT AAATCAGAGAACAGAAAGAAAATAAGTATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGAGCCCTGGGAAGAGGGATGAGAAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGAAGCCCAAGGAAAGTTAAGT
WI-5898	61 C A ---	---	---	TTCTATTTAAATCTGTGCCCATTTGCAAGACTGCAATTCAGTCTGCATGAGCCTTAGTTTC/A/TAA AAGCCCTCACACCGAGGGACAATGTTCAAGACTAAATGACTGCAGGTGAGCAATTCCTGTATTA TACAACTGGGACCAAGAGATGACTTTATAATAGTGCGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGTGAGTTTATTTAACTT
WI-7461	153 C T ---	---	---	TATTACTAGGTTTCATAGAGCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAACGCTCCTCACTTCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGGAGTGTGTCT/C/TGTTCCCTGTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---	---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAAGTCTGAGGCTTTAATGGTCCCTGTCTTAAC GCTTTTGGTATACCTTCTCTTTCTGAAGACCAACCTTTCAAACCTCAGAACACAGGCAAGATGCAT ATTCTGATGTTTTCAGATGTGACTCTCTACATTCGGAACACTAGATGAGTAGGCTCTCTTCATCT CAATTGAAATTTCTAGAA/G/A/AAACACCTAATTTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	---	TTTTGTTAAGCTTGTGAAGCCACACAGAAGTATCTACTCTCTTTAC/C/TAAAGTGTACTTTGCA TATATTTTATGGGATGATTTCTATCCCTACTTAAGATTTTCTCTCAGGTTAAATATCCATTTCT TTGTCAGGAGTTCTTATTGGCTTCTTCTAAACCCCTAACCATTCTGCTTATTCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	---	GAAACCTCGTTGGCTCAAAGGAAACTGTAG/A/C/JAAATCTTTTTTTTTTTTGTGTTTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGTGATGGCAGCCTGCTCTTTTGTGTTGTTAAATCCTCTAGT GGCAGCTTGC AAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGAGGTTGCTGAAAAG TAGCAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---	---	---	AAGGCCAGTGGGAAAAGCAGACAAAACACTCCAAAGATAC/J/GJAGATATAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTGATGCTGATGAGGGCATGTGAGACCAAAAGACATTTGGGTCT TGAGGTTGAATAGGAGTTTGTCTGGTGTGCTGCCCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAACTGAGGTAGAGTCACAGAAAATTTCA
WI-11152	179 C T ---	---	---	GATCTTTGCGACATGACAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAAGTTAAAGTCTGACCCAGGGAGCTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAGGCTTGTC/C/TJCTGTGACAGAAACATTGAA AACAGCCAGTAGATGCCACTGATAGA

WI-1968	167	A G ---	---	---	TGGTGAGGAGCTGAAGGCTGAAAGATAGTCTCTGCTCTGGTCTTCGTTGGAATGGATGAGTCTCTTTACAAAATTTTCTCTTCCATGGGTGTTATGTTAGATCATGGAGTTGGAAGACTTAGATTCAATTTGGGGCTGTACAGTTTACTGGAAGTTGT[G]GTAAGTTGAGCAAGTGTCTCTTAATGTCTCTCA
WI-4701	198	G A ---	---	---	GCCTCAATGCCCTTCCCTGTAA GGGTTCATTTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAGAAAAATGGTGGCCACTATTGACTTGATAACACCTACAAAACAACACATTAACACTCCTCCCACTCTAACCGCCAAAGTCTACCTTTGGTCTTTTATTCTGCTAATGACCATACTATTCCCAATTAGA[G/A]CCATGTCAATTTTCAGAAAAGCAGTATA
WI-4823	164	C A ---	---	---	TTATCTTTCCAAACCATGTGTGTTTCTTCACATACTTTACGTAATTTAAATCATGTCAATTAATTAATGCACTTACTTGTGGTACCAGACATTGCTTCCAATTGTAAATCCCTAACACAGCAAGCATAACTGATGTCCATCTTTGTATTCCTAAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGTCTTCTCTGTTTCACCTCCTGTATTCCCTATTTCAGCATTCATGATTA
WI-4860	72	A G ---	---	---	AAAAAACAACCTTCAATTGACATTCTAAGAAGATAAGAAAAACAACGATCCCACTGTGTGTTTGCCTTGATT[G]GGAGATAAAACCTGATCTCTAAGAAAATTAACCAAGCAGTACACTAAAAATAGCCTTTGTGTGTGTTTTCAGGAAGAAAGCCAACTCAAGTTGCTAAGAAAATAATGTTTCATATCACTCTAACTTCCACATAGAGCAATTAATATAGCA
WI-9705	111	C A ---	---	---	TGAAAGGACCAGTTCGAATGCTTACCAAGTAAGTAATCGGAGGGGAGGAAGTAGGAGTTGCTTCCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGCTGCC[C/A]AAAAATTGTTAACACTGATGCTGTCTACAAACGACACATAGAAATCGGTGTAGATTGCGGTCTCTAGTAAGTAGCTAATGTTTAGATA
TGR-A004Z48	177	A G ---	---	---	TGATTGTTGAATTATTGTTGCTGTGTTCTTGGTG CAAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTGTAAGGTGGGCGAGGTGGACTGAAGATCTGTTGGCAGGCTCAGAGACGCGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCATCTTGGGCAATACGGTTATCCCGTGTCTTCATACGCCACAGA[G]TCTCCAAATTCAGGGGCTCCC
U17579	34	T G ---	---	---	GTGGGATGGTGGAGCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG GGGATTCATGTGTCTGTCTCATCCCAATAGCACT[G]CATGACCTCAGCCCCATACTCTTTCTTCCC TATGTTCCAGAGACAGAAATAGACCTGCCCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAGGACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTCTGGGATCAATTTCTATGGGAGCC
WI-7747b	88	T G ---	---	---	TGGGAGAGGGATCCTTTCTAGTTGA GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTCGTTAACTGTGTATGTACATA TATATAATTTTAAATTTGATT[G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCTTGTAAAGTT ATTTCTGTTTGTGTTTGGGTATCCTGCCAGTGTGTTGTAAATAGAGATTGGAGCACTCTGA GTTTACCATTGTATAAAGTATATAATTTTATGTTTGTGTTCTGA

WI-7747a	44	T C ---	---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGCT/CJTTCGTTAACTGTGTATGATAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAACAGCTTCATGCCCTTTGTAAGTT ATTTCTTTGTTGTTGGTATCCTGCCAGTGTGTTGTTAAATAAGAGATTTGGAGCACTCTGA GTTTACCATTTGTAATAAGTATATAATTTTTTATGTTTTGTTCTGA
WI-7189	197	T C ---	---	---	TCCAGAAATTTCTCTTCAGCTCATTTTGTCTCTCTCAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCATTATTTCCCTTCAAAACAATAATTTTACAGAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTTGTTATTTTATATTAAAGCCTACAACATTTT/CJAG TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTATT
WI-7850	57	G A ---	---	---	AGCCGAGCTGGACTCATGGATGTCACCCCTTTGCTCCCTGCTCTTTCTGCCCTGG[G/A]CTCATGTA TCTGCGCAGCTCTGGTACCCCTCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCCCTTGAAGCT GAGAGGCACAGGCAAGGAGCCAAAGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGGCTGCTACTAGAGCC
WI-7907	69	G C ---	---	---	CTCTCTTCATCCCATCACCCCTAAATAGGTCAAGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G[G/C]AGAAGTGAAGGAAGATAGGAAGGATATTACCTCTCTGTTATTTTAAAGAAACATTGTTT GGTGGCAGCAATCCCTGTCCTATCACTGTTAGAGGCCCTAAATTTATATCTATAAATATATAAAA AGCAAGTCAAACTTGGATGATCAAGGTAAATTTTGTCAAAGTTTAAAT
WI-7919	242	T C ---	---	---	GAAGGCAGCTGGATCACTTCCGCGAGTCTTGGGCGAGCTTTGCTGTGGAACACGAGAGCTCCTCT CAGGGGCTGGCACTCACCTTCTATTCTGTATGATGATTGTTGGTTAAACACTGTCAAATAATAGAGAT GTGCCAGATTTAGATTTCTTACCCCTAACTGTTTAAATTTGTAACCTTTATTCATTTGAAAGTGTC AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAT/CJACAACCTT
WI-7928	101	T G ---	---	---	CTCCCTTCTCTATGCTCTCAGCAGCAGTTGGGCGACACTTGTTCATCTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTTCA/TGJACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACTTTAAACCTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCAITAAAAAATACGTACATTTGAGGTAATGGTA
WI-7936	131	T A ---	---	---	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATTAATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATTTCTTGGAGTTAAATGCACATATAGACATACACCAACACTTACACCAACIT/AJ ACTGAATGAAGAAGTATTTGGTAAACCAGGCCATTTTGGTGGGAATCCAGATTGGTCTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	---	TACAGTTCCAGCCGTTGCCCACTCATCTGCGCGCTTTGCTTTTGGTGGGGGCGAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTCATG/TGJAGCCCAAAGTACAGCTGGACCAACCTGGTGTG TGTAAGTAGTAAGATTACCTGAGCTGAGCTGAGCCCTGAGCCCAATGGGACAGTTACACTTGACAGA CAAAGATGGTGAGATTGGCATGCCATTGAAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	---	TTTCTAGGCTGTACAGTCTGATGATGTTTTTTTATAAATATTTTCACTCTTGTAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGT[G]GTTAAAGGATCTCCACAATGCTGCAAGTGTG AAGGCAGTTTCATTGTGGAATAGTTTAAACAGTCAGGAAGCTAAACTGTCAGTATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	---	GGCCAGGAGATTAGCAACAAGGATTCTCTGTACTTACTTGCCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTCTTGCCAGTGT [G]/TCTACTCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACAACACTCAAAAATTGGCAATGTCAATCAG
WI-140	252 C T ---	---	---	ATTGGAAGATTGGAGGGCTTTGCAGAGGAAAAATAGATTTCAAATGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGATCAAGGCTCTAAAGTGAAATGCAAGTTGTTACCAAGTAAAGTTTATA TCTCCATTGAGCCAGCTCATTGGCAGAAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAAATTTAGTTTAAAAATGTGTCAATTTGTCTGTATTGGCAATTCCTTC/
WI-198	218 C T ---	---	---	GAGGTCTTTAGCAACATGGAGCCCTACTGCTTCAACCCGAGTTCGCCGATCAAGTGTGGCACC CATGATGAAACTCTTGCCATGGTTTAGTACCCTGGACCAAGTAGTCAATCCATCCTGACTTTAAAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAAGCACTTCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC/TGTTTAAACAAGCATAGATAATCTGAACAAC
WI-205c	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT/CJCCAAAGGCTTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT/CJCCAAAGGCTTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	---	GAAGACTGAGTTCCAGGAGTTGCAGCCGTTTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCAACCCCAAGTNCCTTCCAAGAGGTCTCAGACTACCTCCTCCATCTCCCT CTCCCCACAACACACAAATACAGAGATTG/CJAATTCAGAGGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACAGAGTAATCTCTTGGTGTCTTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---	---	---	AGCTTTTGAATCCAAAACACATAG/GCTTGACTCTCTTATCTCCTCTTGTGTTAATCTATCC CTGAGGCAGAAATACAGAACACCTGTGGCTGCTGCTGAACGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGCTGAAAGACCTCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCTCTCTGCTATCCCTGATGACTGGGCAAA

WI-276	25 A G ---				AGCTTTGAAATCCAAACACATAGCTTGACTCTTATCCTCCTCTGTTGTAACATCTATCC CTGAGGAGAAATACAGAACACCCCTGTGGCTGCTGACGAGGAGGATGGGGCGGGAGACAT CGGTCAATGTATCAAAGCATCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGAGGGCTTGCTTATCCTCTGCTATCCTGATGACTGGGAAA
WI-427	59 G A ---				TTTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAAATTTAGAACTACTCC[G/A]GTTT TTTCCCTGGGAAATATTCACAAAACATTTGTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCAATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCAITTTATAGAGCCAGGCTTGCTCTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---				CTCTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATATGCCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACAATACTTCTCCACTTCC
WI-562b	106 T C ---				CTCTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATATGCCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACAATACTTCTCCACTTCC
WI-562	103 T C ---				CTCTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATATGCCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACAATACTTCTCCACTTCC
WI-597c	141 A G ---				GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGATATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCTACCAATGTGAGAAATTATTAAC TTGATCTAATATTCTTCACAATAATATACCTGAGAGAAATAAGTCTATTAT
WI-597b	141 A G ---				GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGATATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCTACCAATGTGAGAAATTATTAAC TTGATCTAATATTCTTCACAATAATATACCTGAGAGAAATAAGTCTATTAT
WI-597	136 A G ---				GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGATATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCTACCAATGTGAGAAATTATTAAC TTGATCTAATATTCTTCACAATAATATACCTGAGAGAAATAAGTCTATTAT

WI-811	66 G C ---			TTCAAATTTAACACCATGGGTATATTATAATTTNGCTCTATCCATAGTTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGCTTTGACGTATTACGTATTCGATCAGTCACCCCATCTGGA ACCAAGGTTTCAATTTCTGCTGACCCCTCCCTCTCACCTCTAGCTGGCTCTGACTTCTTCTCTGGGCT GAACCTTCTCTGTGGCTGTCGGCTTCTCTGCTGGCTTGGCTTCCAATAC
WI-811b	156 A G ---			TGAAGCCCTCTCTATACCCCAAGTGCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCAACAGGGGAAAGCACCTTTGTCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGTTATATACTATGGCACCAATTTGGACACAGATTATATATGTCAGA CACCAGNATGTCCTTTAAGATAATGCAAGCAAGCACAAATCTGTCATGGTTT
WI-881	156 A G ---			TGAAGCCCTCTCTATACCCCAAGTGCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCAACAGGGGAAAGCACCTTTGTCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGTTATATACTATGGCACCAATTTGGACACAGATTATATATGTCAGA CACCAGNATGTCCTTTAAGATAATGCAAGCAAGCACAAATCTGTCATGGTTT
WI-867b	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCG/AJTTGTGTTTGGC CAAATAATATCTCCCGAGGACGCTCTTCTTAATCCCTGAAACCTGAGAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTGTCCTCCCAAGCACACATTAGAACTTA
WI-867	113 A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCG/AJTTGTGTTTGGC CAAATAATATCTCCCGAGGACGCTCTTCTTAATCCCTGAAACCTGAGAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTGTCCTCCCAAGCACACATTAGAACTTA
WI-867	119 G A ---			TCATCAGACCTGAGATTGAGCATGAAATCTACCAAGGTACCACAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCACCTACCTCATG/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCAATATGCTGTTTGTACATAA
WI-871b	123 C G ---			TCATCAGACCTGAGATTGAGCATGAAATCTACCAAGGTACCACAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCACCTACCTCATG/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCAATATGCTGTTTGTACATAA
WI-871	123 C G ---			TCATCAGACCTGAGATTGAGCATGAAATCTACCAAGGTACCACAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCACCTACCTCATG/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCAATATGCTGTTTGTACATAA

WI-884	198 T C ---	---	---	AGGTTCTGGACTTGATGCTGGGAAACAAATGGGTGCTGGGAAATTCCTATTTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCGCGATGCAACATTTATTAGTGAAACATGATGAAATGAACATAAT
WI-921b	205 G A ---	---	---	CACITCCCAAGGCTCTGGGGGANGAGCGGTGGGGACGCTGCCGGGAAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-921	205 G A ---	---	---	CACITCCCAAGGCTCTGGGGGANGAGCGGTGGGGACGCTGCCGGGAAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-945c	90 G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTTGTAAGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTGCATAGATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90 G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTTGTAAGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTGCATAGATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167 C T ---	---	---	TTGCTTCAAGAAGTTCTTGCTCAGGAAGTTATTATTTCAGCAACCTAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCT[T/C]TTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	---	TTGCTTCAAGAAGTTCTTGCTCAGGAAGTTATTATTTCAGCAACCTAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATTATGATGTCCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGTTACTTTGGGAGAAATGCTCAACTATAAATAGTCTGACCCCTTCTGTTCTG CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCAGTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAATNTG

WI-1147b	204 GA ---	---	TTGCCATTATTGAAGATAACCCACACACCTTGGTGTCCAGGGTTTTCACAGGTTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCCAGCCACCGCAACTTCTCCTCCTCCCTGCTGGCTC CTGAGCCAAAACAGGCATTACCATAAATCACTTTGTTAGGATGAACCTTATCTGGCCCAAACTGATA C[G/A]GCATGACCCACAGCCTCAGGTATATAAACACTCTCATCAGGCAGA
WI-1158b	147 CT ---	---	GCATTGAGGGTTCGTTAATGACATTCAGTGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCTGAGTGTCTGAATGCGCCAGGTGGC TAAGTCTGGGG[C/T]CTGGGGTCAGGCTGCCTGGGTGCACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 CG ---	---	GCATTGAGGGTTCGTTAATGACATTCAGTGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCTGAGTGTCTGAATG[C/G]GCCAGGT GGCTAAGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTGCACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 TC ---	---	AAGTTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTCCACAGACACTTATCCCTTAGACAGCCATTCTTTTGAATGN[T/C]GNCANT AAAAATGATTGAAATTGGGAATAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202 CT ---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305c	46 CT ---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305b	153 TC ---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAA[T/C]TNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305	202 CT ---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA

WI-1306b	248 A G ---	---	TTCTGCATTGGAATAGTTGACTTCTATGAGNINNGCAATAATAATGGACAATCTTGNGNNNNNG GGCTGGGTGACTGTCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTTGAAGGCCAGTTGAAATTTATCTTCTCTA/G/GC
WI-1306	240 A G ---	---	TTCTGCATTGGAATAGTTGACTTCTATGAGNINNGCAATAATAATGGACAATCTTGNGNNNNNG GGCTGGGTGACTGTCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTTGAAGGCCAGTTGAAATTTA/GJCTTCTTAGC
WI-1307b	118 T C ---	---	GACAAAGGCTGGTACTAGTTTCCAATTCOAATCTATGTACACTTTCCTCTCACITTTCTCAAGTGGACA GATTTTCTGCATTACTGCTGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTT CCTACCCCTCTAAATGTATCTTNCATAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTTGTTTCTCTGTAAAGNTGTTT
WI-1307	118 T C ---	---	GACAAAGGCTGGTACTAGTTTCCAATTCOAATCTATGTACACTTTCCTCTCACITTTCTCAAGTGGACA GATTTTCTGCATTACTGCTGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTT CCTACCCCTCTAAATGTATCTTNCATAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTTGTTTCTCTGTAAAGNTGTTT
WI-1325b	169 T C ---	---	GAGATGGCCAAAGACAAAGCAGAGGGGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCITTTGCTCCTCT/CJACCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATTCACACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGT
WI-1325	165 C T ---	---	GAGATGGCCAAAGACAAAGCAGAGGGGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCITTTGCTCCTCT/CJACCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATTCACACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGT
WI-1327b	162 T C ---	---	CTACGATAATTAGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGAAGAGTCTGTTATTTGTAAA ACACCAAGTGGGTTTATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG/CJGAAGTTGGGTAGTACCAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTACTGAAGAGGCAATGGTCCATCTCTAAG
WI-1327	175 C G ---	---	CTACGATAATTAGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGAAGAGTCTGTTATTTGTAAA ACACCAAGTGGGTTTATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGGAAGTTGGGTAG/CJGTACCAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTACTGAAGAGGCAATGGTCCATCTCTAAG

WI-1341b	136 G A ---	---			TATCAGCATGATTGTGGCTGTGGACACAAAGTCAATTTGTACTTTTGTGNTGCNNNTCTTTTCNNTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTNAATATATACCCCAAGC [G]A]GGATTGTGATGGATCTGTTTATTTCTGTGCTTGGACACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCGAGCCCACTTGCACTTAGCAAGTGT
WI-1349e	192 G C ---	---			CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGAGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTGTGAAATTTCCATCTCTGAGTTCAGAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAATA
WI-1349d	264 C A ---	---			CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGAGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTGTGAAATTTCCATCTCTGAGTTCAGAA ATTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAATA
WI-1349c	192 G C ---	---			CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGAGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTGTGAAATTTCCATCTCTGAGTTCAGAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAATA
WI-1349b	264 C A ---	---			CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGAGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTGTGAAATTTCCATCTCTGAGTTCAGAA ATTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAATA
WI-1349	264 C A ---	---			CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGAGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTGTGAAATTTCCATCTCTGAGTTCAGAA ATTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAATA
WI-1403b	57 C T ---	---			TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCT/TTTCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAGGGTTGATCTGATTGT
WI-1403	58 T C ---	---			TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCT/TTTCCGA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAGGGTTGATCTGATTGT

WI-1417c	31 C T ---	---	CAGCGCGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGGGGCGAGATGTAGCCACCGGG GGTACAGCATGCCTGCTGGCATTGGAGGCCGCCAGGAATCCCAGTGGCCCTCTCAATGACTTG GGTCTCTGACTCGGAAGTTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGCGCGTTGC AGCGAGGCCCTTAGGTCCGTATTTAATGTTTGTGTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---	---	CAGCGCGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGGGGCGAGATGTAGCCACCGGG GGTACAGCATGCCTGCTGGCATTGGAGGCCGCCAGGAATCCCAGTGGCCCTCTCAATGACTTG GGTCTCTGACTCGGAAGTTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGCGCGTTGC AGCGAGGCCCTTAGGTCCGTATTTAATGTTTGTGTTGTAGAAAAAGTCGC
WI-1729	172 A ---	---	CCATGAGCAACAGCATGTTTCTACTCTGTGTGTATGTTAGGGGCGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTTGGAGAACTGAAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGATGTGTCCTTCCGTTGGTACCTTCTCTCCACCACATCACTGTGTTTTT
WI-1732b	122 T C ---	---	TGCCTTACTTCTTGTTCATCCCAACCATACATTTTGTAATTGGAATCTTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGACATATTCAAGGAGTNCCTGGGTCAACCTTT/CJATTCAGTCT CTGCCACATGCTAGTAACTGTGAGTGATGGTGATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTTCACTACTTATCATCATATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1732	114 C T ---	---	TGCCTTACTTCTTGTTCATCCCAACCATACATTTTGTAATTGGAATCTTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGACATATTCAAGGAGTNCCTGGGTCAACCTTT/CJATTCAGTCT CTGCCACATGCTAGTAACTGTGAGTGATGGTGATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTTCACTACTTATCATCATATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1750	97 A G ---	---	GCGAATTTAATGACTCCAAAGGTAGTAATCCTTTCCCAAAAAAGGTTTTTAAATCTGTGTTGGA CATAATGTTTGAATTTGCAGTTCACCTTGGTGGTAAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCTGACTGAG CTACATTCACCTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	GGTACACAAAGAAATGCTTCTGGAAATCTACJAGTAGGCCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAACCATGAAAGCTGGGCAAGAACAAATTCCTAGGAAAGTACAATTAC TGGGAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTTGAGTACAGAGGACATTCAGGAATAATCATAAAAAT
WI-1803c	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATGAGTAGGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTACATATCTCTG GGTGTAAATTTCAATATATCTACTAAAGCATGACTTCTAGAAAAATTAATTACTCTTGTCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATACTGGAATCA

WI-1803b	77 A G ---			CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATGAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTAATTAATCTTGTGCTCAA GGAAATGGGAATACCTATAATACAGTCTTAATGAGGAAAATACTGGAATCA
WI-1837b	112 C T ---			TTTACTGGGATTTTCATAGCTGATCATAATTTACCATTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC/C/TJCTGTCCCCAGTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTAGCTTCTGCTGGCT
WI-1837	112 C T ---			TTTACTGGGATTTTCATAGCTGATCATAATTTACCATTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC/C/TJCTGTCCCCAGTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTAGCTTCTGCTGGCT
WI-1840b	79 G T ---			TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG/TJGAGAACTCTGAATATTCAGACATACAAAGTGTGACACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTCTCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T ---			GGGCTCACTTTTCATCAGAGCACATATCAGTGATAGTGTCTTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTTGAGGTAAGGACCTGCCNTTTA/C/TJGTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAATAGTCTTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCT
WI-1879b	110 C T ---			GGGCTCACTTTTCATCAGAGCACATATCAGTGATAGTGTCTTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTTGAGGTAAGGACCTGCCNTTTA/C/TJGTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAATAGTCTTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCT
WI-1879	110 C T ---			TGTTCTCTGTCAGGACCGGGCTAAGTCTTGTCTGCATAATGAATATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG/C/TJGCTCTGAGAGGT AAAGTGCCTGCCCAACCGGCACAACTAGAGAGGAGCAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTCCATGAGAAACCACTTTCTTGTCTC
WI-1900b	119 C T ---			

WI-1900	119 CT	---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCGATAATGGATAATCAACTGGACACCCCGNG CTNAGGTAGGNTACCTNGGCAATTAGCCCATCTTACAGCTGCGAAAGAGGCTGCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAGTCCATGAGAAACCACTTTCTTGCTCC
WI-1943c	165 CT	---	---	ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACACAGCCCTCTCTGAANCCTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165 CT	---	---	ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACACAGCCCTCTCTGAANCCTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164 CT	---	---	ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACACAGCCCTCTCTGAANCCTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270 AT	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGGGATCTGGAGAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270 AT	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGGGATCTGGAGAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203 TC	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAGGAGTGCA TTCTGGGCATTTCTTCATAGAGTNTTGTGTTTGTAGTCTCGTAATAACTGTTGGCCCTAGGAAGGTTGT TTCTCTACTGCGTCTGTGAAAGCCCTTCCCATCGAGTGATACAGTACTTTCCAGTTATGGAGATTTT /CJTAAACATCAACACTGGCTGAGGCTGTGG
WI-2012	102 TC	---	---	AAATTCAGAGCCAGAGTCAAGTCAAGTATTAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTCTCTTAATTCTGCACAAACTAGCTAAAAATCT/CJTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTGCACCTTTTCTACTCTCAT GGCTTCAACCAATGCTTCCACTGGATC

WI-2013	127 C T ---	---	CTTTAGAGGTGGTCAATTCGGTCCCTCTCTGGAAAGTGATTCTGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAACAGTCTCCAGCAGATAAATGCTGATACTGACACTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAAATGACTTTGTTTCAGTTATGCTCCCGGGTCC CCTTTACTGGAGGATATCTCAGCTTTCTGAGCCCTGTTACTGCAATCC
WI-2032c	166 G A ---	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCAACCAACTGGTTTCTAGATGTACACG/GATGTGGGACCTCTGTCTCAACCTCCGACTTTTCAG AGATCATTGGTAGGCTCACCTTCTGTAAATTGCTTCTGTTTTCAAAGGG
WI-2032b	219 C G ---	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCAACCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GCTTCTGTAAATTGCTTCTGTTTTCAAAGGG
WI-2032	219 C G ---	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCAACCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GCTTCTGTAAATTGCTTCTGTTTTCAAAGGG
WI-2054b	188 C T ---	---	CGTTTCTTCTACATCTTGGGNNACATAAAGANGAAAGAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACGCCAGGCTCAACAGAACTAATACCTGCTTC/TCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2054	183 T C ---	---	CGTTTCTTCTACATCTTGGGNNACATAAAGANGAAAGAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACGCCAGGCTCAACAGAACTAATACCTGCTTC/GTTCCTCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2573d	129 T C ---	---	TGGGATTAACCCCTGTTTCTTCTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACTTCCCGTTCACAAGGTGTTCCGTGCTTT/CJTGGA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCTAGGTAAAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAGGTCAATATGGCTGGGCTTGGACGAG
WI-2573c	165 A/C ---	---	TGGGATTAACCCCTGTTTCTTCTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACTTCCCGTTCACAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACCAGGGCTTATTT/CJTGCTAGGTAAAGGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAAGGTCAATATGGCTGGGCTTGGACGAG

WI-2573d	129 T C ---			TGGATTAAACCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTTCGTCGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---			TGGATTAAACCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTTCGTCGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2573b	165 A C ---			TGGATTAAACCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTTCGTCGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2573a	129 T C ---			TGGATTAAACCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTTCGTCGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2868b	60 A G ---			GACTTCATGCTCATGAACAAGCATTGTCTTAATTACAGACATTAAAGAAAGCTTTCCAGCTC CCACTTCCCTCCCACTATCACTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGCTCCTG ATCATGGAAGCCAACTACTCTATTAACGCTTCCCAATGATGAGCCCACTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAATAATGAAATATCGATATAC
WI-2868	60 A G ---			GACTTCATGCTCATGAACAAGCATTGTCTTAATTACAGACATTAAAGAAAGCTTTCCAGCTC CCACTTCCCTCCCACTATCACTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGCTCCTG ATCATGGAAGCCAACTACTCTATTAACGCTTCCCAATGATGAGCCCACTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAATAATGAAATATCGATATAC
WI-2870b	131 T C ---			CATGCTGTGAACCTCTGTGCTGCTTGTGCTGGGGAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAATGACTGGATAATGATTC AGAAATGAATAGAGCCCACTTTAAATATATACAGCTTTATGTCCACTTCTGTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT
WI-2870	131 T C ---			CATGCTGTGAACCTCTGTGCTGCTTGTGCTGGGGAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAATGACTGGATAATGATTC AGAAATGAATAGAGCCCACTTTAAATATATACAGCTTTATGTCCACTTCTGTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT

WI-2954c	49 T A ---	---	TTAGCACATATCTGTTGTGGGACTTAAGTGAGACAAGGCATAAAAAA/T/AJAGCACCTGGGGCA CAGAGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACATATCTGTTGTGGGACTTAAGTGAGACAAGGC/A/GJTAAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACATATCTGTTGTGGGACTTAAGTGAGACAAG/GTGCATAAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/CJG CTGCCAGCACCAATAAGCTTCTTCAAAACAATTTGTAACTCCTCTCTCTTAATAAACCTAAG ATTTCCTTGTCCCTGACATTCTGAAGCCACCGTGTAGATGTATGCCAGATTGCAATCCT AGTTCCTTAATGTTATCTGAAGAAAACCTTTTACTTAGGGATTGICT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/CJG CTGCCAGCACCAATAAGCTTCTTCAAAACAATTTGTAACTCCTCTCTCTTAATAAACCTAAG ATTTCCTTGTCCCTGACATTCTGAAGCCACCGTGTAGATGTATGCCAGATTGCAATCCT AGTTCCTTAATGTTATCTGAAGAAAACCTTTTACTTAGGGATTGICT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTJA /TAAATCTTCTTCTGGT/G/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA AATCTTCTTCTGGT/G/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTJA /TAAATCTTCTTCTGGT/G/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151 GC ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 AT ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA /TAAATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995e	151 GC ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151 GC ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA /TAAATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133 AT ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA /TAAATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85 CT ---	---	---	GTGGTGAGTTTCATCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCAG ATCTCACTTAGCTCCTT[C/T]CTGCCATATCCTGTTTCTCTACTCTCTCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTNNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACCTTTGCAAGG
WI-3234b	68 TC ---	---	---	ATTCTGTAATGTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGCCATTACCTTACTTA T/C]GACAAGCAAGAACAAACACAGAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATCTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAATAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTNNATATCTTAT
WI-3234	68 TC ---	---	---	ATTCTGTAATGTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGCCATTACCTTACTTA T/C]GACAAGCAAGAACAAACACAGAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATCTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAATAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTNNATATCTTAT

WI-3292b	106	GA ---	---		GTCTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACCTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGATGGATTGGATGGGATGGATTACTT GCCATGAATATTTCCATTGTTTCTCATTAATGTTAATTAATTAAGTAAATATTTATTNCCATGA GACACAATGGAAAAATGGAAAAACATTCATGGAAAAAACCCATTTCATC
WI-3292	106	GA ---	---		GTCTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACCTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGATGGATTGGATGGGATGGATTACTT GCCATGAATATTTCCATTGTTTCTCATTAATGTTAATTAATTAAGTAAATATTTATTNCCATGA GACACAATGGAAAAATGGAAAAACATTCATGGAAAAAACCCATTTCATC
WI-3355	19	GC ---	---		CCATGAACCATGGGCTACA/GC/ATATTCCTAACTCAGAGTCCCTCTACTGGAGAGGGATCCA CTTTTAAATATGATTCTTGAAGTGGCTGCTACTATTCCTTCCAAGCAGCTTAAACTCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTNNAGTTG
WI-3408	194	GA ---	---		CCATGAAGATGAGTCCCTCCCTCCCTGGGTGACGTCCTAAGATAGCACACCCCTTGAGAAATTNACT TAGCAGTGGCATTGTAATGGCTGATTTCCTCGCTCTAAGACACACCTTTATGCTTTTNAAGCTTT CTGGAATTGGGATGAATCTNACATTCAATGTGCACCTTCGTGTGGGATCCTCTCCG/GATGCCCC ATCTCTGNGAAGCCACTGGGAAGTCGAAGAGTCACTTCAATCAGG
WI-3505b	131	GA ---	---		TAACTTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCAGCTTAAAAAATTATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTCTTACACATTAACCTATTTTNAACCAAC[G/A] AGGTATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATTGGGAAATATGTTTGCATAT
WI-3505	131	GA ---	---		TAACTTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCAGCTTAAAAAATTATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTCTTACACATTAACCTATTTTNAACCAAC[G/A] AGGTATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATTGGGAAATATGTTTGCATAT
WI-3564b	177	CT ---	---		GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGAGAAATAAAAGT GAAATCAATGTGTCTTCCAGTGTATTCACATGGCAGAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGTTC/JAACAAAGTGTGTGTGTCTATC AGTGTACACATGCTACCTTCTTACAAAAA
WI-3564	177	CT ---	---		GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGAGAAATAAAAGT GAAATCAATGTGTCTTCCAGTGTATTCACATGGCAGAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGTTC/JAACAAAGTGTGTGTGTCTATC AGTGTACACATGCTACCTTCTTACAAAAA

WI-3649	64 A G ---	---	AATGTCCATGCTGTGACTGCTACACCTTTCCCTAGTATCCCTTAGTGAAGATTACAC(A/G) AGACCAGTTTGCCTTCACTTAGTAGGGCCCAATGATAGACTTTTAGGTGCTACCAAGGGTACCTGC ACAGCCACATATATGTCACAGTATGGTTGCAAGGACCTGCTAGACTCTTTCTGCTGCTGCTGGTC TTCTGTTTACCATAATTAATGATGACATGCAAACTCAGAGCCTTTTA
WI-3674b	133 G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTAACTACAGCGGAGTCTTTATAGTAATTAATAATGTTTATTTAGAAAAATACAAAAAT[G /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACCTGGTCAAAATGATTGTT AATCTTAATTAATTGTGTTTATGTTTNNATTAGTCCCAATCAGAGCCCAAG
WI-3674	133 G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTAACTACAGCGGAGTCTTTATAGTAATTAATAATGTTTATTTAGAAAAATACAAAAAT[G /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACCTGGTCAAAATGATTGTT AATCTTAATTAATTGTGTTTATGTTTNNATTAGTCCCAATCAGAGCCCAAG
WI-3682	137 G A ---	---	CAATATAGACCAATGACTGCCACAAGAGAAATTAGTGGATCTACATTTAGAAACCACATGTTTTT ATTGGCTCTCTCTCTCTCTCTTTTATGCTCTCTCCACACCAATTCACCTTATCTTTTCAAA T(G/A)AGCATTTGTCCAATTTAAGTCAATGAAAAATAATGTACATTTTCAACAAGTATACATTAA GCCCTGCAAAAGTGCTTATATGCTAT
WI-3854b	194 G A ---	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTTGCCCTTGA CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAACTC TGTTTCAAGGAAGGCAAGGCAGTTATGACCACCTTACAACCTGAGGAAATCAAAGCAAC(G/A)AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194 G A ---	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTTGCCCTTGA CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAACTC TGTTTCAAGGAAGGCAAGGCAGTTATGACCACCTTACAACCTGAGGAAATCAAAGCAAC(G/A)AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210 G A ---	---	AGCCAGCCACATCATGTTGAGTCTGCTCATCTCTCATCTCTTATTTCTCTACTGCCTTCACCTT CCATTAAACAAGAACTCTGTGATTACATTGTAIGTTTGGTTACACTACAGAAATCCAAGATGACCTC CCCATCTCAAGGTCAACTAATTACACCTTAATCTATTTGCAATCTTTTGTCATTACCATACATATT CATGG(G/A)TTCTGGGATAAGGGGTAGACATTTTATGGGAGGCATTAA
WI-4110b	130 T C ---	---	GAAAAATGATGTTTTGATTTCCCTTCTCTATCTTCAGATTATTGGAGTGTGATTAGAAAACTGATAGT AACCTTTTATTGATGAAACTCTGTCTATAATTAAACCTCTCTCTCTCTTTATTTTGCCCTT(C/J)ACA GTTTAGGTAAATAAAGATGCCCCAAGAAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGAGGAGGTGGGGGTTTTCTGGGAAGA

WI-4110	130 TC ---	---	GAAAAATGATGTTTTGATTTCCCTTCCTATCTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTTGATGAAAACTGTGCTATAATTAAACCTTCCTCTTCCTGCTTTATTTGCCJTCJACA GTTTAGGTAATAAAAGATGCCCAAGAAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAAGGGAGGAGGNGGGGTTTTCTGGGAAGA
WI-4119b	168 GA ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTGGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAGGTAACTACGGGGAAGAACAGAGCAAGAACAGACAGAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCIGTTGATCATCATCTCA
WI-4119	168 GA ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTGGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAGGTAACTACGGGGAAGAACAGAGCAAGAACAGACAGAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCIGTTGATCATCATCTCA
WI-4123b	51 TG ---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAAATAGAAAAAGTG[T/G]TTTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATCTTCGTTACATAATTGTATAGAATTTAGTGGGG TTCTCCATGACATTTGGCTTTCTCTCAACAGTGGGTGGTTGGATGTTTCCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51 TG ---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAAATAGAAAAAGTG[T/G]TTTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATCTTCGTTACATAATTGTATAGAATTTAGTGGGG TTCTCCATGACATTTGGCTTTCTCTCAACAGTGGGTGGTTGGATGTTTCCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145 GC ---	---	TTGTACATGTTTCATTCATCCCTCCCATTCCTTTCTGTCTTATAAAGAACCTCGCTTCCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATACT GTGCTGT[G/C]CCTTGTAAGAACCCAGAGCCGAGCATACCAACATGATCTTTTGTGCTGAACGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137 TC ---	---	TTGTACATGTTTCATTCATCCCTCCCATTCCTTTCTGTCTTATAAAGAACCTCGCTTCCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATACT T/CJGTGCTGTGCTTGTAAGAACCCAGAGCCGAGCATACCAACATGATCTTTTGTGCTGAACGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188 GA ---	---	TAACACACTTTTCATTTGGTTTCTTACTGCAAGTTAAAGGACCATCCATTATATTAACAATTCCTC AGTTCTATGCTTTAGAGTNCATATAGGACTACTGTAAATTTTCAGAGGGAAATCTCTTGGAGTA GGGGAATGAGTTAAATATCTACCACATGCCAATTCAGGAGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCTTCCCAAGTTCTTAAATTCCTAG

WI-4230	93 T ---			AGAGACGTTGAATGGGGACATCTTTCTATTTCGATTTTAGTTTAAACATTTGATAAGAATTGATGAAA GTTTGACATTTCCAGATTTATCTTTATAGCAGCAAGCTGGCAATAATAACAGCACACTGACT TTCCATGGTAAAAGAAGTTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTAAATGGAGGAGATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 CT ---			GAAATTCATTGAAGTTTGACCTTGACCTGAACTGATCTCATTAACTTTTNCCTGTAGTGGTTGATTT CATTTTGACAACAGAACAGACGAGAAAATTTCCACTTAAATTAATTTCTCCTTAAAGTATCTATGAT TTAGACTGTTAGCACCAAGAACTGTGAAATTAATCTCTAGATATTTCTCAGAATCTAGGATGGAAG AA
WI-4271b	151 A ---			CAGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGAGCCCCAACCCCTCTTGTCTCAGG CTCTAGAAGTCCAGTCAGGGGGC
WI-4271	151 A ---			CAGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGAGCCCCAACCCCTCTTGTCTCAGG CTCTAGAAGTCCAGTCAGGGGGC
WI-4389b	156 GA ---			AATCGAAACATTGATTTTGTAAAGAACACACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATGATAACCTTTTGA AGGTAAGATGTGAACCTATACA(G/A)TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 GA ---			AATCGAAACATTGATTTTGTAAAGAACACACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATGATAACCTTTTGA AGGTAAGATGTGAACCTATACA(G/A)TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A G ---			GATGACAAATTATTGTGATTGGCATTTTAAA(G/G)GTACCATTCACATTTCTTCTGGCTTTCGTGTGT TGTTGTTGAGAAGTCAGGGGTTAGTCGTATTGCTCTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATTG TATTATCTATGCTTAAATGCTCAG
WI-4491	145 G C ---			ACCATCAATGATCACCTTCTAAAATTTATTAGATGATTAACTGGCTCTGTTAAAAAATAAAACCT GTCTGGACATTGAAAATAAACATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACATA AACAAGTTAAG(G/C)GTTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACTGTCA TTTCTTGTCCTCAATAAATAAATTTTACATGCGCT

WI-4584	144 A G ---	---	TTGGTGGCATTAGCCTCATAACAACTATTTACAATCATAAATGTTACTCTTATTTTACAAACAAG AAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCAAGATTGAAACCAGGAATCCATT CACCGTACIAGTGTCTACCTGGTAAAAAATGTTTAAATAAAACTATGGCATTAGATTTCAAAGA GTCTAATGTGGTTTGAAATAGGTGTGCTTAAATTTGTTATCAGTATGC
WI-4639	185 C T ---	---	TTCTGCATTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCAATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTCCAAATCCACCATTAC TGACCATATGACTTGGGAACATTATCTCACCTATCTGAGTCTGATCC/C/TTCATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATAATTGTGAGGATAAAATGAAATAA
WI-5327	63 A ---	---	AAATGAATCCGCTTAGAGCAATACCAGTAAGGGCTGGTGAGGATGGTGGCTGAGAGA/A/- JGATTACTATAAAGCATAATTAATTTATAAATATGGAATTTAACTAGATAAATTAATGTGAAT TGAGTTTGAAGTTGCATGAGAGTAGGAGGAGTAGTTCTACTTATAGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCGGATGACATGATGAATGTTCTAAGCAGACAG
WI-5390	87 C T ---	---	GCCTTGAGATGAAAGGGGAGCCTGGACCATTGCAGGGCTCTTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTTATC/TGCTGTCTCCCTCTGTTGTCATGAAACAATGAATTC OCCAGTGCCTGGCCGATTTCGGCTCCTAGAGGTGCCAGAAAAAAGTTTCGGTGAATGAATTG ACGAATGGGTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87 G A ---	---	CCCTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTATTTAATTTG/AJAAAGAACTGTTTCTGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTCATAACAA
WI-5404	87 G A ---	---	CCCTGCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTATTTAATTTG/AJAAAGAACTGTTTCTGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTCATAACAA
WI-5545b	77 A C ---	---	TAGGAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTTCTCACCACCTCACACTGCCGCA TATCTGCTC/A/CJCCAAACACCTCTGTTTCTGACAGCCCAAGTTCCATCAGTTGATATGGGACTATT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATTGAATTTTATTTTCATTCA
WI-5545	77 A C ---	---	TAGGAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTTCTCACCACCTCACACTGCCGCA TATCTGCTC/A/CJCCAAACACCTCTGTTTCTGACAGCCCAAGTTCCATCAGTTGATATGGGACTATT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATTGAATTTTATTTTCATTCA

WI-5860b	134 A G ---	---	---	ACTCAAGTTGGGGGATAAAATCAGAAGTTTCTATGTACAACCTTAAATTTTGCTAAGATTTTATTGT TTCITTTTATATAAATTATGGAATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTAC/A GJTATACCTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTTCCAAATCATCAACTCTGTAT
WI-5860	134 A G ---	---	---	ACTCAAGTTGGGGGATAAAATCAGAAGTTTCTATGTACAACCTTAAATTTTGCTAAGATTTTATTGT TTCITTTTATATAAATTATGGAATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTAC/A GJTATACCTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTTCCAAATCATCAACTCTGTAT
WI-6106	208 C G ---	---	---	GCAACAACCTATTATACCTGATCCAAACCCAGGTCTACTAACATTAAATCAACCCCTAACCAATAC TATATATTGCTCTGTTCTGAATTTATTTAGAAATCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTCTCCAGGAGTCTCAATGTGAAGTATAATCTTACAGAG TAATT[C/G]ATAGTAGTACCAACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCT[C] AAACCTATATTNCTGTCTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAATAATTATCCCTGAAATTTTATACCA
WI-6109c	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTAA ACCTATATTNCTGT[C/G]TGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAATAATTATCCCTGAAATTTTATACCA
WI-6109b	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTAA ACCTATATTNCTGT[C/G]TGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAATAATTATCCCTGAAATTTTATACCA
WI-6109a	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCT[C] AAACCTATATTNCTGTCTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAATAATTATCCCTGAAATTTTATACCA
WI-6112	96 T C ---	---	---	AATGCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAAACACATGCTGTTTGTCAATGAT[C/G]GATATCCCAAGTGCCTTAGACAATGCCTCCCATAC AGTGAACAGATTTTGACTAAACATACCTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCGAGG GAAC

WI-6244	103 T C ---			TAATTGCACAACCTTACATATCAGGGTTTCTGATTGAAGAAGAGATAATCCCTTTTAGTGATT GCTTAATAATTAATTCATAATAAGTGCACCATCTCTT[CGCTCCTTATAAATGTGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAGCAACCAGGAGACATTTTTATATACTCTACAGTGGGGGAAGACTT CCTATTTCTTCCCAGGATGATACATTCTAC
WI-6268	124 C T ---			CTGGCCTTATAATCCAAGTTTAGGATTAATCTTACCCCAACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAGATTCTCCTAGTAGGGCTTGGGTGTGGCACCGTTGGCTCATTC[CTIACCTCTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAAGAGCTGGACAAAACCTGCTCTTTTCAGAAAGAGTCG GGGTCCAAAGATTTCGTACGATTTTITA
WI-6336b	234 C T ---			AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCOC ATATAATCCCCCTTACATGTTTTCTTATAAGACATACAGTTTAACTAAATTAACAAAACTAACACGCTT ATATACTGGCAATATATACAGATGGGTTATGTCAGAGTATAGATCACATGAAATGGACCATGTG GTACCCCAAGTGCATTATGTCTTGGTAGAGCC[C/T]TGAGGACACTGACAGT
WI-6336	234 C T ---			AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCOC ATATAATCCCCCTTACATGTTTTCTTATAAGACATACAGTTTAACTAAATTAACAAAACTAACACGCTT ATATACTGGCAATATATACAGATGGGTTATGTCAGAGTATAGATCACATGAAATGGACCATGTG GTACCCCAAGTGCATTATGTCTTGGTAGAGCC[C/T]TGAGGACACTGACAGT
WI-6381	92 C A ---			TGGAATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAAATAGTTATGAGTATTTATACAATTA CAAAAATGGNTTCATGTTTTAACAA[C/A]GTATTTTAAAGCTCAACACATTTTAAACACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTTGAATGTCTCACTCCCAACTCCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAG
WI-6436	198 C G ---			GGTTAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAAATGGACATTTTAGGAAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAGGCTTAGGAAGACAGTAGTCTCTGTGTTGAA ATTTGGTGTCTATAATAAGAAGTTTAGACTTTGGTGGTTGTAGTAGTTGTAGTAGAGTAGCGGTT[C/ G]ATTGGGTGATTCCACAGACAAGGTGATGTTCTAAGATTTGATATTATTGT
WI-6449	186 C T ---			GAGGCCTCTTTGCTTTTCCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTTCTGATTGGTTGGTGTGCTCACACTGCCAGATTGTTAAATATTTTGAAAAATC GTATCTGGTTCTATTCACTGCACTCTCTGATCTTATGTCTGGCTATT[C/J]ATCOOCTATTCTCTGA TCITATGTCAGACCTGAAGTTCCCTCTAAATTTTCTGGGTGATTATA
WI-6449	186 C T ---			GAGGCCTCTTTGCTTTTCCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTTCTGATTGGTTGGTGTGCTCACACTGCCAGATTGTTAAATATTTTGAAAAATC GTATCTGGTTCTATTCACTGCACTCTCTGATCTTATGTCTGGCTATT[C/J]ATCOOCTATTCTCTGA TCITATGTCAGACCTGAAGTTCCCTCTAAATTTTCTGGGTGATTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAAGACCTCCAAAGAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACAT/CTTGAAAAAAATTTAAAGTAGAACTCAAGAGCCAAAAGTCCCAATTTGTGCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTTCTCCTCCTC CAGTCCCATTTATATGACATTCGGCATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCCATCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAAIC/TTGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAAGAGTGAAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCCATCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAAIC/TTGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAAGAGTGAAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACCTCAATTAACCTTTCACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCAGCTTCGAGGCCGTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGAGAAATCAGAGT/TA/GCTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACCTCAATTAACCTTTCACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCAGCTTCGAGGCCGTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGAGAAATCAGAGT/TA/GCTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTTGAATGCAACTGAGAAAATGTTTNTAGGCCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TAGCAATATCTTA/G/ATCAATTTTAAAAAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAATAATTGTGCAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTACCCAGGCCCACTGTTCTATGCG/A/CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCATTGATTATNATTTTGTGGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA
WI-6584	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTACCCAGGCCCACTGTTCTATGCG/A/CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCATTGATTATNATTTTGTGGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA

WI-6608b	46 C	---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/- JAGTTCAGGCAGCTAAAGGAGGGGATTCCICCTAGTCCCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTAATTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACAGAAAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/- JAGTTCAGGCAGCTAAAGGAGGGGATTCCICCTAGTCCCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTAATTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACAGAAAAAGGAA AGC
WI-6666	68 C A	---	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTCCAAAAAGGAAACCTCCCC A[C/A]AAATCCCATCAACACAGTCATGCTGGAAGGCATTCTGTCTTACTCTGTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGCCCTCTCTNTCTCAAGTCCAGGCTTCTGGGTAGACCACAAACTA ATACACAATGTTAGGCACACAAGAGA
WI-6670b	120 A G	---	---	AGATTAAACATAATTACTGGGCCATTGTAGGGTNGGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTAGCCA GCATTGCCATTGAGGCGGAGTCAGGGTTGTGGGCCAGAAAGTTAGACAATTTGGGGAATCTGA AAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT
WI-6670	120 A G	---	---	AGATTAAACATAATTACTGGGCCATTGTAGGGTNGGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTAGCCA GCATTGCCATTGAGGCGGAGTCAGGGTTGTGGGCCAGAAAGTTAGACAATTTGGGGAATCTGA AAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT
WI-6704c	33 T C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAACT[C/C]AACATCATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---	---	---	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTAGAAATAACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACACATTTTGTACAGCTGGAATGATCCCG(G)ATAGTAAACTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTATTACTGAGTCGACACAGGATGTACCAGTGAGCCTC ATCTCCAGTCCAAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ---	---	---	AAACAAATGGTGCAATGCAATAATTGGGTCACAGTATAAACAATAACAATTAGTTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN(G/C)AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAAATCCAGTTCCTCTTC
WI-6766	148 G C ---	---	---	AAACAAATGGTGCAATGCAATAATTGGGTCACAGTATAAACAATAACAATTAGTTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN(G/C)AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAAATCCAGTTCCTCTTC
WI-6787b	97 A G ---	---	---	ACAGATAAAGTCTTTATCCCTGTATGTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAAATTCAC(G)TTTTTACTGCATAAGATATCTTCATGTACAACCTGT ATGCTTTGCTCTCTTGGGAAGGACGCTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGAATAGGGCAGAGTAGANTACTCACAGGAAAAGAGTAAATTCAGGT
WI-6793	105 C G ---	---	---	GAAACCAACAGGTCCTGTTATTTTATTAAAGGAGCATTTACATTTAGTAAAGTTCACACATTTCA TCAACAAGGCGGCTTCAAAATCAATCAGTCAACCCCG(C/G)GAGTTAGAAAGTAGAGTCATGAGGAA GAGTGTCTGGCTGTAGGAAGTAGGGTTAATGCCCTCTAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTTCTCATCACAGGTAAAGGCAAC
WI-6810b	37 T C ---	---	---	CACAATAATAAAATCACTCCCTACCTTGAACCTTTAT(C)JAGAAGCATTTTTTAAATTTACAACACA AAGCTCAACGACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTTAAAAATGCTATGNACAAAGTACAATTTCTTTTGAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---	---	---	CACAATAATAAAATCACTCCCTACCTTGAACCTTTAT(C)JAGAAGCATTTTTTAAATTTACAACACA AAGCTCAACGACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTTAAAAATGCTATGNACAAAGTACAATTTCTTTTGAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---	---	---	GCATGATTAACCCAGTGCAGAAAATACCAAGTACATTTGGGTGAACGATGAGCTAGCTGTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAATCAACAATGTAGCT GCAGGGTAAC(C/A)GTGGATACCCGTGTGTCTACTNGCCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTCAATCTTGGTTCAGGTGGCGCTGTGCAG

WI-6817	145 C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATAGCTAGCTGTTCTAGTA TTTGGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/A]TGTGGATACCCGTGTGCTACTNGCCCTCCAAAGGCATTCAGGGGATCATCA AAGTGTGGACACCTTGTTCAATCTGGTTCAGGTGCGGCTGTGCAG
WI-6819b	221 C ---	---	GATGAAAGCCCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTAC CATCATGTCAACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCCTAGTAAAGCCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTG CTTAGCAAAACAGCAATAACTTTTGTGTTCCCTATATGACACCTAATATCCAG
WI-6819a	175 G T ---	---	GATGAAAGCCCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTAC CATCATGTCAACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCCTAGTAAAGCCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTT[G/C]ATATACAAAATTTTCTGCTATT TTGCTTTAGCAAAACAGCAATAACTTTTGTGTTCCCTATATGACACCTAATAT
WI-6826b	154 A G ---	---	GCAAAAGCTTTATGGCTCCCAACAAATATCCCTTTTAAACTCCCTCTCTCTCTGCTCAGTG GAACAACACATTTTGAATTTTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACGTG TAAGCTGAATTCGAAATATGGAACACACACACTGGACTGGGTATACGTTG
WI-6826	154 A G ---	---	GCAAAAGCTTTATGGCTCCCAACAAATATCCCTTTTAAACTCCCTCTCTCTCTGCTCAGTG GAACAACACATTTTGAATTTTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACGTG TAAGCTGAATTCGAAATATGGAACACACACACTGGACTGGGTATACGTTG
WI-6857a	122 T C ---	---	AGTGCAAACTATTTTGAACAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTCACATAAGTAAATACAGCAGATGAGATGICICACATGAT[C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTAGTCAACTTTTCAGTGTAAATTCACAAATATAGCAGCTCA AACACAAATGCAGGAGCAATGGCAAGTTTGGCAACTGTTTGGGCTAAT
WI-6865	153 G A ---	---	TTATAGAATACTTATGGGGCATACGNGTAAATGAACGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTGGTTCGTCCTGAAATCCCTCCCTGCTCACAACAGCCAGCTACNGGTTTCTTAAAGACGTA ATTTTGCAGGCAAACTTC[G/A]TAGAGCCATTCGTGTCAGAGAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTAGAAGATATCTTTGCGCTGTAGAACTGAGCTCATTAA
WI-6909	73 C T ---	---	ATTGAAAACCTGTTAGCAACAGATAAATTACAATAGAGCCCTGGATATAAAAATGAGAGAAGATGC AGACTTA[C/T]AAGCTTATAGAGAAAAGTCAAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCAACAGGATTATTCGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATAATTGGATGCCCTAGTTGCCCTATTTTATACATAIC

WI-6996b	242	G T ---				ACTTCTAGTGCCCTGTTACCAACCACCTTAATGCCCTCTGGTCGCCGCACCTTCTGATGTCCGTAGGCCCT TAAATCTGCCTGGCGTCCCCTCCTCTGCTTTCAGCACCCAGAGGAGAGAGCCGCGCAGTTCOCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTTCC[GT]GTCGGATC
WI-6996	228	T G ---				ACTTCTAGTGCCCTGTTACCAACCACCTTAATGCCCTCTGGTCGCCGCACCTTCTGATGTCCGTAGGCCCT TAAATCTGCCTGGCGTCCCCTCCTCTGCTTTCAGCACCCAGAGGAGAGAGCCGCGCAGTTCOCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTTCCGGTCCGGATC
WI-7021b	112	G A ---				TGGGAGGACAGGGGAGATGCTGCAGTTCCTCAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTCT CTGAAGCTCCCTGCTCTGAAAGCCACAGACAATAATGGTCCCCAAT[GA]CCCCGACTGCACCTTCTGTG CTTCAGCTCTTGTGACATCAAGGCTCTCCGTTCCACATCCACAGCCAATCCAAITTAATCAAACC ACTGTTATTAAAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A C ---				TGGGAGGACAGGGGAGATGCTGCAGTTCCTCAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTCT CTGAAGCTCCCTGCTCTGAAAGCCACAGACAATAATGGTCCCCAAT[GA]CCCCGACTGCACCTTCTGTG CTTCAGCTCTTGTGACATCAAGGCTCTTCCGTTCCACATCCACAGCCAATCCAAITTAATCAAACC ACTGTTATTAAAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T ---				GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATGCGGGTGG COCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAACCGTTGGTGAC[CT]GGTGGGAGCCTCT GGGGCTGTTGAAGTCACTTGTGTGTTCCAAAGTTTCCAAACACAGAAAGTCATTCCTTCTTTTTAAA ATGGTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118	C T ---				GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAACCGTTGGTGAC[CT]GGTGGGAGCCTCT GGGGCTGTTGAAGTCACTTGTGTGTTCCAAAGTTTCCAAACACAGAAAGTCATTCCTTCTTTTTAAA ATGGTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153	A C ---				AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGICICTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACGCTCTATAAATAGTATTCCTAACATCACTGTG CTTAATTTAAATAGCATTT[A/C]TCTTATCATTTATCAGCCTTTTATGTAATTTTCCAAAGTAAAAATATTA ACATAATTATTCATTGGTCTCTTTTTTATCTGGTCTATATGAATGCTAT
WI-7091	153	A C ---				AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGICICTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACGCTCTATAAATAGTATTCCTAACATCACTGTG CTTAATTTAAATAGCATTT[A/C]TCTTATCATTTATCAGCCTTTTATGTAATTTTCCAAAGTAAAAATATTA ACATAATTATTCATTGGTCTCTTTTTTATCTGGTCTATATGAATGCTAT

WI-7136	58 T C ---			TGTGAAGCCACATTTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTTATTGAAC TGTC/AAATTC TCTCAATAACTCAGTGTAGCACITTTAAAGTCTGAAGGACAGCAACATGAAAAGAGCATATCAATGTG GTGGAGAAAAGGGAAGGGTGGCTTTTAAATTTATTTTCTTCATCTTTTATAACAAGAAAGNNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTCTATATAIG
WI-7146c	210 A G ---			GGGACGCCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTCGTTTAGCTG AATAATGAGTTGTTCTTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCCCAAGCCCATGCCCTGCCG TGGTGCAGCTGGGCTGTGGATGGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGCGATGCG AACGC[A/G]GTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7146b	210 A G ---			GGGACGCCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTCGTTTAGCTG AATAATGAGTTGTTCTTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCCCAAGCCCATGCCCTGCCG TGGTGCAGCTGGGCTGTGGATGGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGCGATGCG AACGC[A/G]GTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7146	202 G A ---			GGGACGCCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTCGTTTAGCTG AATAATGAGTTGTTCTTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCCCAAGCCCATGCCCTGCCG TGGTGCAGCTGGGCTGTGGATGGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGCGATG/A JCCAACGCAGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7153	161 A T ---			ATATTACAACTTGCTTTTGTAGCTGATCTTCCATCCTCAAAATGACTCTTTTCTTTATATGTTAACATA TATAAAATGGCAACTGATAGTCAATTTTGATTTTATTCAGGAACATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAAACNNNNNNN[A/T]AAAAAAGTTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAATGGTATGTTT
WI-7155	156 T G ---			TAGAATAGATGCGGTCAATCTCTTTGGCTTCGGTCTCCAGCCCTCATGGTTGGCATCACATAT GCCGTCATGCCATTACACCAGCTGGCCCTACCCCTATAATGATCCTGTCCTAAATTAATATACAC CAGTGGTTCCCTCCCTGTT/G]TAAAGACTAATGCTCAGATGCTGTTACGGATATTTATATTCTAG TCTCAGTCTCTGTGTCACCCCTCTCTCTCTCTCCGCTCCCAACTCCAG
WI-7169b	161 A G ---			AGCTCCACCCAGATGCAGATTGTGTTTGTGTTTCTTGTATCACTGTACACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGCTAGCCCAAGCCCATCAAGTCTGAAATTCATATTTGGTTTATGCAAAAT ACAGCAAACTTTTATTTAAGTAGAT[A/G]GGAGAAATATGTTTAAAAATATTAGGAATCCTAGACCATA TTTTCAGGTCACTCTAGCAGCTAGGATTCTCAATGGGAAGTATATATA
WI-7175b	194 C T ---			CTCCTAGACTAGTGTCTTACCTTTTATTAATGAAGTGTACAGGAAGCCCAAGGCAGTGTCTCCACCA ATAACTTCAGAGAAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCAATTGTCCTAGCCTA[C/T]AGAT AATTTATTTTGATTTTGAATAAAAAACATTTGTACATTCCTGATACIGGG

WI-7216c	237	T C ---	---			TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTGTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAAATCTCAAGATTCCCTCCAGAAAAATACGTATGT TTAAAAACCTTCTCTGCTATACATAGGAAAAGACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTTGTITTTTTCCTTGTAATCACTT
WI-7216b	237	T C ---	---			TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTGTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAAATCTCAAGATTCCCTCCAGAAAAATACGTATGT TTAAAAACCTTCTCTGCTATACATAGGAAAAGACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTTGTITTTTTCCTTGTAATCACTT
WI-7220b	147	A T ---	---			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCATTATTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATTCTGGCTTACGTCACATAATTAGTGTIT
WI-7220	140	A T ---	---			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCATTATTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATTCTGGCTTACGTCACATAATTAGTGTIT
WI-7226	232	C ---	---			GATCGAATTTTTCAGATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATGTATATA TACATACACTCCTATTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTGATCATTT CCCTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAATAATAA TTACCCACAAATGCCACCAGTAACATTACGATCTTCTGAGTTT
WI-7228b	254	G A ---	---			ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAAGTAATGGCTCCAATTCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTCTTGTCTTTGTAATCTATTTAGTTGATTTAATTA CTTCTGAATAACGGAAGGATCAGAAGATATCTTTGTGCTAGATTGCAAAATCTCCCAATCCACA CATATTGTTTTAAATAAGAAATGTTATCCAACTATTAAAGATATCTCAATGTT
WI-7228a	163	G A ---	---			ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAAGTAATGGCTCCAATTCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTCTTGTCTTTGTAATCTATTTAGTTGATTTAATTA CTTCTGAATAACGGAAGGATCAGAAGTATCTTTGTGCTAGATTGCAAAATCTCCCAATCC ACACATAATTGTTTTAAATAAGAAATGTTATCCAACTATTAAAGATATCTCAA
WI-7233c	213	C T ---	---			CGATCGTACTGCCAGTAGCATTGCTGTCTGCTCGGCTGTGTTGTACATTCATTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCATAATTATTTAAATTTATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTTACTTCTCTTCCACCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAGTATCTGTGCACAAAAACCACTGCCAGATAACCAAGAGGGGCTGTG

WI-7233b	213	C T ---	---	---	CGATCGTACTGCCAGTAGCATGTCTGTCGCGGCTGTGTTGTACATCCATTTCATTTCAATTGTTACA GATGTGAACITTTATTCCTGTCACTAATATATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTCTTGCCACCCTTTTGCGCAATATTAAAGTGAAGTCTGCTAATA GTGTAAAGTAC/TGTGTCACAAACCACTGCCAGATAACCCAGAGGGGCGCTG
WI-7233	211	T C ---	---	---	CGATCGTACTGCCAGTAGCATGTCTGTCGCGGCTGTGTTGTACATCCATTTCATTTCAATTGTTACA GATGTGAACITTTATTCCTGTCACTAATATATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTCTTGCCACCCTTTTGCGCAATATTAAAGTGAAGTCTGCTAATA GTGTAAAGTAC/TGTGTCACAAACCACTGCCAGATAACCCAGAGGGGCGCTG
WI-7238	128	T C ---	---	---	GGGTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACACITTTTGTCTTAGICITTTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTTT/CJCCGTT CTGTTTAAACAGAAATAAAGGAGTGAAGCTCCTTTCTCATTTCAAAGTTGCTACCAAGTGTAT GCAGTAATTAGAACAAAGAAACATTTCAGTAGAACATTTTATTGCCTA
WI-7252f	520	T C ---	---	---	CCACAGGATCCAGCCAAAGCGGCCCCCTCCCGCCCCCTCCACTCGCAGACGCGCGGGACAGAG GCCTGCCCGGGCGGCGCAGCCCCGGCCCCCTGGCTGGAGGCTGCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGGCTGGAGGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCCTCCTCCA
WI-7252e	552	T C ---	---	---	CCACAGGATCCAGCCAAAGCGGCCCCCTCCCGCCCCCTCCACTCGCAGACGCGCGGGACAGAG GCCTGCCCGGGCGGCGCAGCCCCGGCCCCCTGGCTGGAGGCTGCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCCTCCTCCA
WI-7252d	540	T C ---	---	---	CCACAGGATCCAGCCAAAGCGGCCCCCTCCCGCCCCCTCCACTCGCAGACGCGCGGGACAGAG GCCTGCCCGGGCGGCGCAGCCCCGGCCCCCTGGCTGGAGGCTGCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCCTCCTCCA
WI-7252c	552	T C ---	---	---	CCACAGGATCCAGCCAAAGCGGCCCCCTCCCGCCCCCTCCACTCGCAGACGCGCGGGACAGAG GCCTGCCCGGGCGGCGCAGCCCCGGCCCCCTGGCTGGAGGCTGCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCCTCCTCCA
WI-7252b	540	T C ---	---	---	CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCCTCCTCCA

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WI-7252a	520 T C ---			CCACAGGATCCAGCCAAAGGGGCCCTCCCGCCCCCTCCACTCGCAGCAGCCGGGGACAGAG GCCTGCCGGGGCGCGCAGCCCGGCCCTGGGCTGGAGGCTGCCCGGCCCTGGTCTCTGGTCOG GACACTCTAGAGAACGCGAGCCCTAGAGCCCTGCCGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCTGGAGGATGCGAGGTGGAACCTCAGTCACTAGACTCCTCCTCCA AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTTT
WI-7265m	252 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265l	231 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121 T G ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227 T C ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT GTTTAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170 T G ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATTCGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231	T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCATTCGTGGTTCAITGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATTAATGTAATAATAACGATCTCT AAAAATACCACAGTTTGATTTTCTTTT/AAGGAGTAAAGATTTGCCT
WI-7265e	227	T C ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCATTCGTGGTTCAITGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATTAATGTAATAATAACGATCTCT AAAAATACCACAGTTTGATTTTCTTTT/CCTTAAGGAGTAAAGATTTGCCT
WI-7265d	174	T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCATTCGTGGTTCAITGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265c	170	T G ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCATTCGTGGTTCAITGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265b	121	T G ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCATTCGTGGTTCAITGTAT GTTTAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265a	80	T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCCATTCGTGGTTCAITGTAT GTTTAAGGAAACCAAGCATATAGATGCAATAGTATTTTGTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7281b	183	C ---	---	---	GATCACCCAGCCACAGCCCTCGAGGGCCCTATACCATGGCCACCCTTGAGCAGAGAGCCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCCTTGGCAAAAACGGAGTCCGCGAGGCCGCGAG GTGTTGTGAAGACCACACTCGTCTGTGTTGGGTCTGCAAGAGGCCCTCCTC
WI-7281	171	C A ---	---	---	GATCACCCAGCCACAGCCCTCGAGGGCCCTATACCATGGCCACCCTTGAGCAGAGAGCCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCCTTGGCAAAAACGGAGTCCGCGAGGCCGCGAG CAGGTGTTGTGAAGACCACACTCGTCTGTGTTGGGTCTGCAAGAGGCCCT

WI-7282b	159	G C ---	---	TGTCACCTGGCACATTTCATTTCTCAGTTGAAGAAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCACCTCAAAAATATGTCAACTTNNNNNNNNNT AGGCCCTTTCATAAAACCAAACTG/CJTAGCAAGATGCAAAATGCATGGCAAAATCTGTGGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C ---	---	CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTGTCCCAATTAATCTCCCCACTCCACTAC TCTCTCCCTCCACTTCATTTTCCT/CJTGTGCTTCTCTCTAATTCAGTGTGAGGCTGACTTG GGGACAAACGTAATTATGATATTAATGCTGTCTTCTCTCCCAATAGAAGAAATAGTCATGGAGCC TGAAGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGACCCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTG A/GJCGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGAAATACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301e	94	T G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGACCCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTG TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGAAATACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301d	138	A G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGACCCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTG CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGAAATACAGTGGACAACAGCAATCA AATTATGGAC/CJCATGAAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301c	211	A C ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGACCCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTG CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGAAATACAGTGGACAACAGCAATCA AATTATGGAC/CJCATGAAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301b	182	C T ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGACCCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTG CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGAAATACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301	88	G T ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGACCCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGAAATACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG

WI-7301	205 A C ---			AACTATGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGGTGGAGGATATGATGTTACATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAACAGCAATCA AATTACITGGACACATGAAGGGGGCAGTTTGGTGAAGAGCTCGGGCAG
WI-7314c	49 G A ---			CTCTCCTTTTCTTCAGATCTGCTCCTGGTTTAAATTTGGGAGGTCA[G/AJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGTAAATGAAGTCAATTAATAAATTTCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACTATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7314b	49 G A ---			CTCTCCTTTTCTTCAGATCTGCTCCTGGTTTAAATTTGGGAGGTCA[G/AJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGTAAATGAAGTCAATTAATAAATTTCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACTATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7314	36 A G ---			CTCTCCTTTTCTTCAGATCTGCTCCTGGTTTAAATTTGGGAGGTCA[G/AJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGTAAATGAAGTCAATTAATAAATTTCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACTATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7321b	199 C T ---			ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGAGTCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGTCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ---			ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGAGTCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGTCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---			AGACATTCTCGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCOCTGGC TCCAGTGAAGTCTGGGCATGCTCAGGCTACTATAGGTCCAGAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAAATCTGAATTTGGGATTTTCAAAGATAATATTTACATACACTGTATGT TATAGAATCTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[AC]CA
WI-7338c	221 A G ---			CTCTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTTATTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATCAAGACTATCTGCAGCTA GTGTGTTCTTCTTACACAG[A/G]TATACACACAGACATCAGAAAAATTCGTGT

WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAAGAAATATTGGCAAAAGGTGCTTTT[A/C]CCTTG AGCCATTATTGTGTCAGAGAACAAAGAAAGAAAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTGTGTCAGAGAACAAAGAAAGAAAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTTCTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATTCGT
WI-7338	221 A G ---	---	CCATGTCAATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACITTTAAATACCATTAATACATTTGATTTTCAATTTGTAACACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTTTATTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACITTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384c	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACITTTAAATACCATTAATACATTTGATTTTCAATTTGTAACACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTTTATTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACITTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACITTTAAATACCATTAATACATTTGATTTTCAATTTGTAACACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTTTATTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACITTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384	145 T A ---	---	TGAAATCCTGGGTCCTTGGCCTGCTGAGTGGTTTATTTTACITTTGCCCTCCCTTTT TGAGATCCATCCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTTGCAACAAGGTACCTCTATTTCGCCACAAGCGTCTCGGGATTGTTTGA CTTGTGCTGTCCCAAGAACTTTTCCCTCCCAAGATGTGTATGTTATGG
WI-7388c	106 A T ---	---	TGAAATCCTGGGTCCTTGGCCTGCTGAGTGGTTTATTTTACITTTGCCCTCCCTTTT TGAGATCCATCCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTTGCAACAAGGTACCTCTATTTCGCCACAAGCGTCTCGGGATTGTTTGA CTTGTGCTGTCCCAAGAACTTTTCCCTCCCAAGATGTGTATGTTATGG
WI-7388b	106 A T ---	---	CTTGTGCTGTCCCAAGAACTTTTCCCTCCCAAGATGTGTATGTTATGG

WI-7388	94	T A ---	---	TGAATCCTGGGTCCTGGCCCTGCTGCTAGCTGGTTATTTTACITTTGCCCTCCCCACCTTTT TGAGATCCATCCTTTATCAAGAAAGT/AJC/TGAAGCGACTATAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTTACCTCTATTTTGCCACAAGCGCTCGGGATTGIGTTGA CTTGIGCTGTCCAAAGAACTTTCCCCCAAGATGIGTATAGTTATTGG
WI-7438	64	A G ---	---	TTAGATTTAATTGGCAACCAGCAACTCACTGCCACCATCCACTGCAGATCTNCTATTCTGG[A/G] GTTGATATGACAAGGAAACCCTATTGGAACCAAGTCTCAGATTGNCATGTCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTACTGTAAACATAGTTTGNCCTGTTATTGTTA TTGGAATGAATATCGCTTCCACTGACITTTACCA
WI-7454b	152	T C ---	---	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGCTACTTCTCAAAATGTTTTGACA
WI-7454	152	T C ---	---	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGCTACTTCTCAAAATGTTTTGACA
WI-7464c	177	G C ---	---	AATTTGAAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAAATAATTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTAATTTCTCTATGTA CAACAGAGCCACAGCACAGAGGGTGGCATAAGCAGTTGCCA[G/C]CCAGAAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGGAAGCAACGTTCAACCAACAATTAT
WI-7464b	168	C A ---	---	AATTTGAAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAAATAATTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTAATTTCTCTATGTA CAACAGAGCCACAGCACAGAGGGTGGCATAAGCAGTTGCCA[G/C]CCAGAAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGGAAGCAACGTTCAACCAACAATTAT
WI-7464a	103	C A ---	---	AATTTGAAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAAATAATTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTAATTTCTCTATGTA GTACAACAGAGCCACAGCACAGAGGGTGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGGAAGCAACGTTCAACCAACAATTAT
WI-7499b	134	T G ---	---	CAATTCATCAATCCAACCTAGTCTGNTGCTTAAACCATTCAGACAAAACCTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTCAIT /GJTATAGTCCCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGA ACTCTGTACAAAATTCCTTTTGAAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33 A G ---	---	---	CAATCTCAATCCAACCTAGTCTGNTGCCCTAA[A/G]CCATTCCAGACAAACTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTC ATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTTAGGAA CTCTGTACAAAATCCCTTTGAAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	---	TGGGAATAGTAAGAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAGTAGTCTGGTCTGATTCCTAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAGAATGAGTGAAGAGGAGGAAAAATCATGATGTCATGATGCAGTAATTACTATGTCA GAAGAAAATATTTAAAATATTGGACCACCTCTTGTTTACCATCCCTACCCACT
WI-7506	118 A C ---	---	---	TGGGAATAGTAAGAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAGTAGTCTGGTCTGATTCCTAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAGAATGAGTGAAGAGGAGGAAAAATCATGATGTCATGATGCAGTAATTACTATGTCA GAAGAAAATATTTAAAATATTGGACCACCTCTTGTTTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTTATGCCCTTTCGGGGTTCTTGATGTTCGCAGTGCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGAACACATCCCGGTGATAGAATTGCT AAATTGTC/TG/GTGAATAGGTAGAAATTTTCTTTAAATATGTTTTCTTATTCGTGAAAAATTCGG AGAGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---	---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTTATGCCCTTTCGGGGTTCTTGATGTTCGCAGTGCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGAACACATCCCGGTGATAGAATTGCT /CJAAATTTGTCGTGAATAGGTAGAAATTTTCTTTAAATATGTTTTCTTATTCGTGAAAAATTCGG AGAGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTTGAAC TAGATTGCATGCTTCCCTCTTTGCTCTT[G/A]GGAAGACCAGCTTTCAGTGCACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCCCTCGGCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTTGAAC TAGATTGCATGCTTCCCTCTTTGCTCTT[G/A]GGAAGACCAGCTTTCAGTGCACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCCCTCGGCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTT/CJCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCAGCTAAGTCTCGATTCTGTTAAAGCCACTTGGGTG ATAAGAAAGGGAAGTAAAAATGAAGTCTGACTAGAAATTCATTTCAGAGGCCAAGTACATTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTCATTGATGTGCAATTTGAATTTTCAG

WI-7555b	60	T C ---	---		GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTT/CJTCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCTGATCTCTGTTAAAGCCACTTGGGTC ATAAGAAGGGGAAGTAAATAATGAAGTCTGACTAGAAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTTCAG
WI-7555	60	T C ---	---		GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTT/CJTCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCTGATCTCTGTTAAAGCCACTTGGGTC ATAAGAAGGGGAAGTAAATAATGAAGTCTGACTAGAAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTTCAG
WI-7567b	290	G T ---	---		TGAGCCATCACTAGAAAGAAAGCCCATTTTCAACTGCTTTTGAACCTTGCCTGGGCTGAGCATGAT GGGAATAGGGAGACAGGGTAGGAAAGGGCGCTACTCTTCAAGGGTCTAAAGATCAAGTGGCCTTGG ATCGCTAAGCTGGCTCTGTTGATGCTATTTATGCAAGTTAGGGTCTATGATTTAGGATGCGCCTAC TCTTCAAGGCTAAAGATCAAGTGGGCTTGGATCGCTAAGCTGGCTCTGTT
WI-7569b	63	T C ---	---		AATGTATCCCTTTCCGTTCCAAACAACAGGAACCTGACTGGGAGTGAAGGAAGGATGGCA(T/C) AGCGTTATGTGTAATAAACAAAGTATCTGTATGACAACCCGGGATCGTTTGAAGTAACTGAATCCAT TGCACATTTGTGAAGGCTTAAATGAGTTTAGATGGGAATAGCGTTGTTATCGCCTTGGGTTTAAATT ATTTGATGAGTTCCACTTGTATCATGGCCTACCCGAGGAGAAGAGGAGTTTG
WI-7574c	216	A G ---	---		GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTTGCCAAAGGCCAAAC TCCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACITACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC(A/G)TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216	A G ---	---		GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTTGCCAAAGGCCAAAC TCCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACITACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC(A/G)TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216	A G ---	---		GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTTGCCAAAGGCCAAAC TCCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACITACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC(A/G)TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7576c : 168	A T ---		---		AATGATGATGATAATGATGATGACGACGACACACGATGATGCTTGTAAACAGAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAAATTTTGAAGGCGGCTAGTTGACACACTTTGGAAGTTTGTGT TCTGTTTGTAAAAACTGGCATCTGACACAAAAAA(A/T)GTTGAAGGCCCTTATTCTACATTTACCTAC TTTGTAAAGTGAGAGAGACAAGAAGCAAAANNNNNNNNNNAAGAAAAATAAAC

WI-7576b	168 A T ---	---	---	AATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTTGGAAGTTTGTGT TCTGTTGTTAAACTGGCATCTGACACAAAAAA[AT]GTTGAAGGCCCTTATTCTACATTTTCACCTAC TTTGTAAGTGAGAGAGACAAGAACGCAANNNNNNNNNNAAGAAAAAATAAAC
WI-7577q	77 T C ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCA[TC]CAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAATAATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTACAC[GT]AGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAATAATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---	---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTAC[GT]ACGTAGGAAGAAAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGIGGCCGTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117	A G ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTA[G]ACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77	T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50	G C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157	G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACAC[G]ATAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48	A G ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84	G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93	T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154	C A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTA[C]ACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577b	117	A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATTAAGTTTCTCTGAGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577	107	G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATTAAGTTTCTCTGAGTA/GJTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7619q	106	C G ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTCTAATTAC ATGCGAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCCATCTTTTCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150	T C ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228	A G ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCCATCTTTTCCCTC CGCTTTCTTCTTACACAGAAACATTA/GJACATACCGAGAAACCTATTTC
WI-7619n	237	G C ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCCATCTTTTCCCTC CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99	C T ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189	T A ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G ---	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCGCGCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCT CGCT/GTTCCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G ---	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCT CGCTTTCTTTTACACAGAAACAT/GCACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCT CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---			ACAAAGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---			ACAAAGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGC[T/G]TTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---			ACAAAGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---			CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGC[A/G]TTAAACCATCATGGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCCCTTGGACTGTTC
WI-7626c	155 C T ---			CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATGGACCAAAATGTG TACTAATGATGAGCAATTTAG[C/T]ACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCCCTTGGACTGTTC
WI-7626b	28 T A ---			CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAG TAATCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATGGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCCCTTGGACTGTTC
WI-7626	144 T C ---			CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATGGACCAAAATGTG TACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCCCTTGGACTGTTC
WI-7689c	134 A G ---			TCCCATACCGCTGATCTCAGGGTCTGTGCTGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGAGCCACCCAGCAAAAGGTTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGAGCTGTACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAAATGGATTTATTAGAAATTCATATGAC

WI-7689b	134	A G ---	---	---	TCCATAACCGCTGATCTCAGGGTCTCTGCTGCGGCCACCAGATGGGGAAAGCACAGGTGGGC TCCCAGTGGTCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCAGCAAAAGTTGTTCTCTAAQA /GTAAGGCAGAGTCACACTGGGGCAGCTGATACAAATGACAGCTGTGTAAAAAGAGAGCTTAAT GATAATATTGGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7689	121	G A ---	---	---	TCCATAACCGCTGATCTCAGGGTCTCTGCTGCGGCCACCAGATGGGGAAAGCACAGGTGGGC TCCCAGTGGTCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCAGCAAAAGTTGTTCTCTAA AATAAGGCAGAGTCACACTGGGGCAGCTGATACAAATGACAGCTGTGTAAAAAGAGAGCTTAAT GATAATATTGGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7690	45	G A ---	---	---	TGGAGAACATTCATCTTGCCTGCTACTTATCATCAATGAAGATTAG/AJCACTGAGATCCAGAGGG CTGGATGACTTGCTCAAGTTCAACAGCATGGTAGTGGCAAGAGAGGTCCAGAGTCTCGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATAGGGCCACCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACGTGCTGATCC
WI-7703b	164	T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTCJAAGTAAATGGTCTCTCACTGTTTATTTAACCTCTAAATTCCT TTCAATTTAGGGTAGCAATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156	T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTCJAAGTAAATGGTCTCTCACTGTTTATTTAACCTCTAAATTCCT TTCAATTTAGGGTAGCAATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---	---	---	TAAATGAGTGTGTTGTACCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGGCCACAGCACTAAAGCAGTGGAC/CJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCAGCTCTCAGOC
WI-7743d	275	C T ---	---	---	TAAATGAGTGTGTTGTACCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGGCCACAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCAGCTCTCAGCCAACG
WI-7743e	106	C A ---	---	---	TAAATGAGTGTGTTGTACCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGGCCACAGCACTAAAGCAGTGGAC/CJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCAGCTCTCAGOC

WI-7743d	275 C T ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTGCTACCTCACTGGGGTCTCTGGGGCTCGGAGCCCTATCCGAGCGAGGTTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743e	106 C A ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTCTGGGGCTCGGAGCCCTATCCGAGCGAGGTTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743d	275 C T ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTCTGGGGCTCGGAGCCCTATCCGAGCGAGGTTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743c	106 C A ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTCTGGGGCTCGGAGCCCTATCCGAGCGAGGTTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743b	275 C T ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGGTCTCTGGGGCTCGGAGCCCTATCCGAGCGAGGTTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	106 C A ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTCTGGGGCTCGGAGCCCTATCCGAGCGAGGTTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	275 C T ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGGTCTCTGGGGCTCGGAGCCCTATCCGAGCGAGGTTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	275 C T ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGGTCTCTGGGGCTCGGAGCCCTATCCGAGCGAGGTTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7758	144 A G ---			TGACATTTATTCAAAGTTAAAGCAACACATACAGAAATTAAGAGGATCTGTTTAAACATTTCC TCAGTCAAGTTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTTCAGAGACATCAAGTG GAGAGAAATC[A/G]TAGTTTAAAGTGCATTAATAATTTTAAACAGAAATTAAGTAGATTTTAAAA GATAAATGTGTAATTTGTTTATATTTTCCCATTTGGAGTGTAACTGACTGCC

WI-7765b	126	G C ---	---	ACAGGGCCCTTGGCAGGTGCAGCCCCCAGCTGCTTTGACCTGCCCTTCATGCATGGAAATTCOCCT TCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG[G/C]TTAGG GAAACATTCATCCTTGAGTCAAAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTG ACTCAAAACCAATCAGTGAACCTTGCTGAGCCTGTAAATATAAAGGTCGGA
WI-7773b	237	C G ---	---	TTAATTTACTGATCCAGCAAGACCAATCATTTGTATCAGATTATTTTAAGTTTATCCGTAAGTTT GATAAAAGATTTCCTATTCCTTGTTCTGTGTCAGAGAACCTAAAGTGTACTTTGCCATTAAAGGCA GACTAGGGTTTCATGCTTTTACCCCTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTTT GATTTTCGACGTTTGACTAGCCATCTCAAGCA[C/G]TTTCGACGTTTGA
WI-7774b	170	T C ---	---	TGCAACCTCTTTTCGTGATGGCAGCCTGCTGGTCAGCAGCTCCAGTAGCGAGAGACGGCACCCAGAAT CAGATCCAGCTTCGGCATTGATCAGACCAACAGTGTGTTCCCGGGGAGGAAACACTTTTAA TTACCCCTTTGCAGGCACCACTTTAATCTGTTT[C/G]ATACCTTGCTTATAAATGAGCGACTTAAA A'GATTGAAAATAATGCTGTCTTTAGTAGCAAGTAAATGIGCTTGCT
WI-7785c	165	G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCCGCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAGGCTAATCCAATTATTATCACAATTACCA TAATTTATTGTCCATTGATGATTTATTGTAATGTATCTTGIGCTG
WI-7785b	165	G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCCGCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAGGCTAATCCAATTATTATCACAATTACCA TAATTTATTGTCCATTGATGATTTATTGTAATGTATCTTGIGCTG
WI-7785	156	T ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCCGCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAGGCTAATCCAATTATTATCACAATTACCA /NNNNNNNNNGCCAGGCTAATCCAATTATTATCACAATTACCATAATTTATTTTGTCCATTGA TGATTTATTGTAATGTATCTTGCTG
WI-7789c	84	G A ---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGGACCCTTACAGAGACTCTCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGAATCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84	G A ---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGGACCCTTACAGAGACTCTCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGAATCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73 GA ---	---	TGCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACG[G/A]TGGAATTTAAGTTTAGGGTCCCTAAAAGCATTTGACACACAGATGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCCTAGGATAT GCCCTCCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190 CT ---	---	AATTGTCAGTCACCTCTTCAAAACCTTACAGTCCTTCTTAAGGTACTCTTCAATGAGATTCAATCCATT TACTAATACTGTATTTTGGTGACTAGGCTTGCCCTATGTCTTATGTGACTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/TT]TCTATACCTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190 CT ---	---	AATTGTCAGTCACCTCTTCAAAACCTTACAGTCCTTCTTAAGGTACTCTTCAATGAGATTCAATCCATT TACTAATACTGTATTTTGGTGACTAGGCTTGCCCTATGTCTTATGTGACTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/TT]TCTATACCTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81 CA ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCTTGGCTCATATTTCTTTTCTTCAT CTTGATGATGAT[C/A]GTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTTCTCT TAATAAGCCCCACATATAAATGTACTTTTCTTCCAGAAAAATCTCCTTGAGGAAAAAATGTCCAAAA TAAGATGAATCACCTAATACCGTATCTTCTAAATTTGAAATATAATTTCTG
WI-7795	81 CA ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCTTGGCTCATATTTCTTTTCTTCAT CTTGATGATGAT[C/A]GTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTTCTCT TAATAAGCCCCACATATAAATGTACTTTTCTTCCAGAAAAATCTCCTTGAGGAAAAAATGTCCAAAA TAAGATGAATCACCTAATACCGTATCTTCTAAATTTGAAATATAATTTCTG
WI-7814c	41 GA ---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGIGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATAATGGGATTTTC TTTTCTTTCTCTGTTAATTTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGIGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATAATGGGATTTTC TTTTCTTTCTCTGTTAATTTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGIGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATAATGGGATTTTC TTTTCTTTCTCTGTTAATTTGACTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	---		GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCAACACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAATGTACACATTCGCAATTTTGATAAAATTAATTTGTTTCCCTTTG AGGTTGATCGTTGTGTTTGTGCTGCACATTTTACTTTTTTGGCGTGGA
WI-7830c	54	G A	---		GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCAACACATTTCTATGCCAAACAGGAAC ACGATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTTGATAAAATTAATTTGTTTCCCTTTG AGGTTGATCGTTGTGTTTGTGCTGCACATTTTACTTTTTTGGCGTGGA
WI-7830b	134	G A	---		GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCAACACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTTGATAAAATTAATTTGTTTCCCTTTG AGGTTGATCGTTGTGTTTGTGCTGCACATTTTACTTTTTTGGCGTGGA
WI-7830	44	A G	---		GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCAACACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTTGATAAAATTAATTTGTTTCCCTTTG AGGTTGATCGTTGTGTTTGTGCTGCACATTTTACTTTTTTGGCGTGGA
WI-7865e	25	C T	---		CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATTCAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCATGTATGTAAGGAAAGTGTATTCACCCAGTAAACCCAAA
WI-7865d	191	C T	---		CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATTCAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCATGTATGTAAGGAAAGTGTATTCACCCAGTAAACCCAAA
WI-7865c	25	C T	---		CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATTCAGTCTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCATGTATGTAAGGAAAGTGTATTCACCCAGTAAACCCAAA
WI-7865b	191	C T	---		CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATTCAGTCTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCATGTATGTAAGGAAAGTGTATTCACCCAGTAAACCCAAA

WI-7865	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG[C/]AAATGAGGCGAGGCAATTC TAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAGATTTCAGGGTGCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAGCAAAATGAGGCGAGGCAATTC TAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAGATTTCAGGGTGCTTCCAACTGAAATCTCAATGTCTCAGTA[C/]GAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7867c	92 A C ---	---	---	TTCAACACCTGCTTCACCCCTCCGACCATCTGTGCAATCACCTTCAGCCCTCAGCTAGTCCCG CTAACAATTACCCCTGCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGTTTAATATGGC CTGTTGAGTTTAATGTTAATGTTGATTTCTTTAAGTAACCAATTCCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ---	---	---	TTCAACACCTGCTTCACCCCTCCGACCATCTGTGCAATCACCTTCAGCCCTCAGCTAGTCCCG CTAACAATTACCCCTGCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGTTTAATATGGC CTGTTGAGTTTAATGTTAATGTTGATTTCTTTAAGTAACCAATTCCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ---	---	---	TTGATCGATCTTTCCACCCCTGTCACCTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGCTCCCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAAATTTCCCTGCTTACCCCTATTCAAGCA[C/]TTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173 C T ---	---	---	TTGATCGATCTTTCCACCCCTGTCACCTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGCTCCCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAAATTTCCCTGCTTACCCCTATTCAAGCA[C/]TTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66 T C ---	---	---	TTGATCGATCTTTCCACCCCTGTCACCTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT /C/TCACCCAACTGCTCCCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACAC AATCATTTAATTTCCCTGCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7870b	85 T C ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCCATAGAAAGCACTAATTAATCTGTCAGTATTAGAAGGG GTGGGTGGCGGGAATCC/T/CJATTTATCAGACTCTGTAATGAATATAAATGTTTTACTCAGAGGA GCTGCAATTCCTGCAAAATGAATCCAATCAGCACTAGAAATTTTAAACATCATTAATGCCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG

WI-7870	76 C T ---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGTGG[C/T]GGGAATCCTATTATCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGAG CTGCAAAATGCTCTGCAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG
WI-7889c	54 C ---			TTAGGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCCGGGCGCAGGGCCTCT GGCTTCCCTGGCCAAATCCTCCCTGGAGAAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAAGGCTGTCTTCTCCAGAGCACAAAGAAG
WI-7889b	54 C ---			TTAGGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCCGGGCGCAGGGCCTCT GGCTTCCCTGGCCAAATCCTCCCTGGAGAAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAAGGCTGTCTTCTCCAGAGCACAAAGAAG
WI-7894c	142 A G ---			AGCCACCCCCAAATATACTGTTATCCAGAAAGCTGTTATGTCTGTTCCTACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCTTATTGTTTGTGAATTTATTTGCGTATAC ATTATC[A/G]ATGTAATAATTTGCATTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---			AGCCACCCCCAAATATACTGTTATCCAGAAAGCTGTTATGTCTGTTCCTACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCTTATTGTTTGTGAATTTATTTGCGTATAC ATTATC[A/G]ATGTAATAATTTGCATTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGGCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGGCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGGCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC

WI-7900d	128	C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84	C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128	C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84	C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128	C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84	C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGGCCATGCTAGAAGTACATTCTCTCAGATTGAAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33	C T	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTTGGGGTGGCTGGGTATTGGGGCAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901b	33	C T	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTTGGGGTGGCTGGGTATTGGGGCAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTGTCATACAGACAGGTAACCTAGTTCT

WI-7901	33 CT ---	---	AGACTTAGGTACAATTGCTCCCTTTTATATACTAGACACACACAGGACACATATATTAACAG ATTGTTTCATTCATTCATCTATTTCCATATAGTCATCAAGAGACCACTTTTATAAACATGGTAAGAC CCTTTTAAACAACTCCAGCCCTTGGTGGGCTGGTGGTATTTGGGCGAGCGCGGTGGTGGT CACTCAGTGGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTCT
WI-7901	271 TG ---	---	AGACTTAGGTACAATTGCTCCCTTTTATATAACAGACACACAGGACACATATATTAACAGATT GTTTCATTCATTCATCTATTTCCATATAGTCATCAAGAGACCACTTTTATAAACATGGTAAGACCCT TTTAAACAACTCCAGCCCTTGGTGGGCTGGTGGTATTTGGGCGAGCGCGGTGGTGGTGGT TCAGTGGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTCTGGT
WI-7926c	150 CA ---	---	CATCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTATTTGGGAATGCCCTTCAIT TACAAATGCAATACCTA[C/A]ATTTAATACTCTTGTAGGAGAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGAA
WI-7926b	28 AT ---	---	CATCCGCATCTGTCAACCCAGGACAGAAATJGATGGACAAGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTATTTGGGAATGCCCTTC ATTTACAATGCAATACCTA[C/A]ATTTAATACTCTTGTAGGAGAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGAA
WI-7926	150 CA ---	---	CATCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTATTTGGGAATGCCCTTCAIT TACAAATGCAATACCTA[C/A]ATTTAATACTCTTGTAGGAGAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGAA
WI-7947b	203 GT ---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACAAACCAATAGCAGCCAGACCCACAGGCGCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCCAGCCAGGACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTTGTCTCAATTCAAATCCATAGATTTGGAAGCCACA GA[G/J]TCTCTCTGAGCAGCAGACTATGGCAGCCAGTCTGCCACCTG
WI-7947	203 GT ---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACAAACCAATAGCAGCCAGACCCACAGGCGCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCCAGCCAGGACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTTGTCTCAATTCAAATCCATAGATTTGGAAGCCACA GA[G/J]TCTCTCTGAGCAGCAGACTATGGCAGCCAGTCTGCCACCTG
WI-7963b	145 T/C ---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTAAAAATAAAATGCC ACAAAATTCATTTCTCTCTTAAGTATTACAATGGAGTTTATCTCTGCTCTAAAAAGTGAAGAAAT TGAGTGAATGA[T/C]AATTTTGTAAATTTAGGATAAGATCCAAAGTATTTCCCAACTCTTGTTCCTC CCATAAAGTTAGGCATGAGGAGGAGCACTCATTAAGGCGAGAGCGGAA

[illegible]

WI-8021b	57	C T ---	---	ACAACTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAC[C/T]GATCCC ACGCTTAGAACCTTCACCACAAGGAGTTTCTTGAGTAGTCTCAAAGTCTGGTAGGCATTCGA ACTGGTCCTTTCACTTTGAGATCTTTCTTTGCGCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTGTAGGGGTGATTCGAATTCGGTGAATGCCA
WI-8021	57	C T ---	---	ACAACTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAC[C/T]GATCCC ACGCTTAGAACCTTCACCACAAGGAGTTTCTTGAGTAGTCTCAAAGTCTGGTAGGCATTCGA ACTGGTCCTTTCACTTTGAGATCTTTCTTTGCGCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTGTAGGGGTGATTCGAATTCGGTGAATGCCA
WI-8024c	206	A G ---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCAGTGGCACTTCCATGGGAAGACAGAAGAGAGT GGGCCCCAGAGATGGAAGACCCAGTGTATCACCACAACCACTTTCAGCCGCTCTAGCCTCTAA TTCC[C/A/G]CTCTAGAACAGCTGGCCCTGGTCTCAGTACACAAGGAAGAGC
WI-8024b	206	A G ---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCAGTGGCACTTCCATGGGAAGACAGAAGAGAGT GGGCCCCAGAGATGGAAGACCCAGTGTATCACCACAACCACTTTCAGCCGCTCTAGCCTCTAA TTCC[C/A/G]CTCTAGAACAGCTGGCCCTGGTCTCAGTACACAAGGAAGAGC
WI-8077	167	A G ---	---	GAATGAGCCTTCCTAGCGCGAGGGACCTGCTGCTGTTGTCGCTGCAGTGCATTCATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAACTCCTTTCT AAGGAGCTGGGTGTCATGCCCTACAAACC[C/A/G]TAAATTTCTCATCAGATGGATTTTATTAACTTT GTGATTGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGGAAAA
WI-8118f	114	G C ---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTGGAAATGACACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAAATGAGCTTGTTC[C/T]TTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G ---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTGGAAATGACACTCCCTTGCTAAGGAAGCTAT TATGTACTTCATGCTGTGGAACTGGCAATACAGAAATGAGCTTGTTC[C/T]TTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G ---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTGGAAATGACACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAAATGAGCTTGTTC[C/T]TTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 CT	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANITTTGGATTTTGGAAATGAIC/TCACCTCCCTTGCCTAAGGAAGC TATGTACTTTCATGCTGTGGAACACTGGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCCTTCCCT AAAAATCAGACTCAITGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 TC	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANITTTGGATTTTGGAAATGACCCTCCCTTGCCTAAGGAAGCTAT GTACTTCATGCTGTGGAAC/TCJGGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCCTTCCCT AAAAATCAGACTCAITGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 CT	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCACACA TTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 AG	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGJTGCGCAGCAGGGCCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 AG	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGJTGCGCAGCAGGGCCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 TC	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCACACA TTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 GC	---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTCTAAGGG/CGJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTTCTACTTCTGACCTATTCAATAGGGGTAAACCACT
WI-8314	78 CG	---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTCTGJTAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTTCTACTTCTGACCTATTCAATAGGGGTAAACCACT

WI-8321	178 GA ---	---	TTTTAAATATGCCCGTTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGTTACTTTTCAAGAGCTGCTGTTATAGTCTGAGTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAITG/AGTATCTTAGTATCTTCTTA TTTGTCTATGGTCTAGTTTATCAACCTACTTTATAGCTGAACGTGTGGC
WI-8321	178 GA ---	---	TTTTAAATATGCCCGTTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGTTACTTTTCAAGAGCTGCTGTTATAGTCTGAGTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAITG/AGTATCTTAGTATCTTCTTA TTTGTCTATGGTCTAGTTTATCAACCTACTTTATAGCTGAACGTGTGGC
WI-8332b	123 AC ---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCCAAGTCTTCCCTCCCTGTGCAGCTTAGA/ACJACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAAGAAATGCCTACTGGAGCTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114 AC ---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCCAAGTCTTCCCTCCCTGTGCAGCTTAGA/ACJACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAAGAAATGCCTACTGGAGCTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311 TC ---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATATCATGGCAGAGGCGGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGAGGAGAGTCTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCAATTAGA AACTGCCCCCATGATCCAATCACCTNTCACAGGCCCCCTCCTCCAAACACGTTGGG
WI-8378	308 TC ---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATATCATGGCAGAGGCGGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGAGGAGAGTCTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCAATTAGA AACTGCCCCCATGATCCAATCACCTNTCACAGGCCCCCTCCTCCAAACACGTTGGG
WI-8426	184 TG ---	---	TTTAGCACATATTTAGCATTAGCCTCAAACGATACAGCAATATGTTACATTCTCTTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNAAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNITAA GAGGNTTCTTTGCTGTGGANGGGGTGGCTTTCGTTGAACCTCCATTCTGT/GGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCCGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61 CA ---	---	TTGAGCCTCCACAATAATGCAACCAAGTTTACATTTTAAACAGCCCTCTACATACACTGCA/CA TCTTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTTAAGA AAAAACCTTCCAGTTATTGTGAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTGAT

WI-8450g	55 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCJTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCJTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCJTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTTC/AJCA TCTTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ---				CAAGGAAAGCTGTCAGTCTTCATAAACTTTCAAAGAGTTACAAAAATACGTAATTTTAAAGJCTA CAATTCAGATTAGCATCCAAACCTACAAACATGATGATACATTCGTCACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATGTTTATACCTTGTAAGAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCAATTTTATJNNNNNNNNCCCTTGCTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAAT/jATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCAATTTTNNNNNNNNCCCTTGCTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAATGCCAATTA TTAGACAAAGAGANTAAATGATATAATATAATCAATTTTNNNNNNNNCCCTTGCTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCAATTTT/jNNNNNNNNCCCTTGCTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGGTAGTACCTTAATTTTGATAAAAAAAT TAAAAAGCAT/jG/jAACATGCATATAAAAAATAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATATCTTCCCTTGTTTGTCTTTTAAAAAACATTATTTCTGAAAAAATAA ATCAGAAAAACATGATCGTGGAGAGAAATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAATCCAGTCTGCAGTCAAGTACCTGT/jTGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTCATAGTTGTCTGAGCTAGAAAACCTGTACCTGTAAAACAAAAG
WI-9439a	76 C T ---	---	---	ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAT/jT/jCCAGTCTGCAGTCAAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTCATAGTTGTCTGAGCTAGAAAACCTGTACCTGTAAAACAAAAG
WI-9446b	75 T C ---	---	---	GAAGGCTTGATTAAGGGAGGNTTATTTGATGTNAACCTACCATTCAGTACTATAAAGANCATTA TAAAAAAAT/jC/jCCTCTAAAGNGACACATGCCCAAATGACCANGNCATAAGCAAAACCTTTAAAT TACTCATCTTCATATGTGTGTTGTNCCCTACTNTTACACTGTGTCTCTGTCTTTTGCTGTACCTA TGNGAACTGCACACTATCTGTGGCAATATGT

WI-9446	75 T C ---	---	GAAGGCTTGATTAAAGGAGGNTTTATTTGATGTAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAT/CJCCCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTCATATGTGTGTTTGTCCTACTNTATCACTGTGCTCTCTGCTCTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185 A ---	---	ATTAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACATTTTTT GAGATAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAGTATGTTAATGTCACCTT GGAATCTACATGGAAAGCCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9497	185 A ---	---	ATTAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACATTTTTT GAGATAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAGTATGTTAATGTCACCTT GGAATCTACATGGAAAGCCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9523b	193 C A ---	---	GTGAAAAGTTTTCTATTCCATCCATACATAGATTGTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAATTACAACTATTTCAAGCCATGATCTATGGTGATTTCCACACATTTGTA/CJAJAGTG AAAGCTCTTCAGCTTGGAAACAACCTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47 G A ---	---	GTGAAAAGTTTTCTATTCCATCATACATAGATTGTGCTAAG/GAJATCATTTTGGAAAGAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAATTACAACTATTTCAAGCCATGATCTATGGTGATTTCCACACATTTGACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGTCAAGGCAGACTGCATGCACATATAT
WI-9554	202 T C ---	---	AAAAACAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAGTGATTATTACCAGAC AAGCATCAGTGATGATAGTACTGCCCTTNTAGTTGTTATGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTACACCCAAAGTACAATATGATAAGCAGCCCTCTGCAGTG GTT/CJGCTGGATACCCTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTT
WI-9555	97 G A ---	---	CCAAAAGCCAAACCATTCATATGATGGATTTTCATAAACAATTTTATGATCCCTTTTGAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/GAJCTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTGAG GGNTAAATGGTACAAAAAAGGCTGTAACTCTTTTNTCTCACATTGATCACA
WI-9625b	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCTCTGGGAAAAACCTTTGGAAAAAACAACGCACACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTCTTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTATTTCATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCTTGGAAAAACCTTTGGAAAAACACACGCACA TAAGTATCAATACTGAGGGTTGGACAAGTTACTTCTATTTGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTAATAAACACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTAGTATGTCTACTATACCTTTTTCATCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTTTGTAACAGTGTATTGCTAGACCTAAAAATCCAAGCT TACAACTTC/TGTCTTTACCTGATACATTTATTCCTTACTTTCATTTGGATTTTAAAAATGTTA ACTTAATAGTCTCTTCAGATGTCCTGCTTTTGTAGTTAATTGTGTTT
WI-9676n	114 A G ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676m	184 G T ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676l	84 A C ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676k	202 C T ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676j	92 C T ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676i	173 T C ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9676h	134	C A ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC C/AJATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTT/CJCCCTCTGTGCGCATGAAATAACTTGA GGCAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC C/AJATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCGC CCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCGC CCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A/C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCGC CCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGATTCTCGGTGCGCTGTGTA[C/A]ATTACAACCTCATTGATCACAATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAATGAGTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACCTTGCCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCCACATGCTGTATTGCTGTCC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGATTCTCGGTGCGCTGTGTA[C/A]ATTACAACCTCATTGATCACAATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAATGAGTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACCTTGCCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCCACATGCTGTATTGCTGTCC
WI-9756	47 A ---	---	ACTGAAATGTAATGGCCAAAGGCCACCCAGGACCTTAAAAATCATAAGAAAGTTAATCTGTGGGAAAA GAGTAACATCAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGCCCCCTTATCATTAGTC AGTAAAGATAAGAAAGCCCTGGTGGTATCCACTCCACAAACACAGAAATATACACTTTTGGAAAG ATTCCACTTAACCATTGATCTTCACTTTTATGATTTAAACCTCCCGTGG
WI-9758	135 A G ---	---	GATGGTCCCTTAAGGATTGCAATTGTTAATGGGCAGACTGGTGCNAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATCAAAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/GTAAATAAATCTCTGGTAGGTTCTATAGCAATGCTAAGTAAAGTAACCGCTGGTTCTCTAAAT ATTACG
WI-9778	127 G A ---	---	ATTTAAATCAGGCAGCGGGGAAAATGGATACTTTCATATGCTGTACCCAACTATAAACTTTTG GTTCTCATGCAACATTTTCAATTTGCTTCTCACTCCAGTACCAGTATTTACCAATIG/AJCTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTTGCCTCA AAGAAATGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCTCCCTTTGCTCTCATGCCCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAAATGCAGTTT[C/A]TGGATCCCAACCCAGGA CTCAAAAAAAGTAGGAATGGGAGAGAGGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101 A G ---	---	TGGAAAAATAGCTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCCTTTTGAATGAATAAAATATAC/A/GTGTGTATGTATATATATATATTAAACACTT AGGATTATATACACACAATAAAACGCTCTGTAAAGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGGTGTGTTACTTGATAIGCTGTG
WI-9880c	222 G A ---	---	GAACATAACACCTTTCTTGCATGGAATTTTCTTGATTATGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTTCTGTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	CA	---			GAACAAACACCTTTCTTGCAATGGATTTTCTTGATTAATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACATATATAAGATCCTCTTTTAAATATATATTTTATATAAGCACAT GAAATGGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	CT	---			GAACAAACACCTTTCTTGCAATGGATTTTCTTGATTAATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATATTTTATATAAGCACAT GAAATGGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	CT	---			ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACTCGGAATCACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTATTTTAAAAACAACGCCCGAGTTATCAGATTTCTNTTTTGTCTC/CACCC ATTTCCATAACAAAAAGAGCTACACAAAAATNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	AG	---			TCCCTCAATGACAGATGAACATAATTTCTCTTGGTGAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA/GJTGATTTTAGATCCTCCCCAG TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	AG	---			TCCCTCAATGACAGATGAACATAATTTCTCTTGGTGAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA/GJTGATTTTAGATCCTCCCCAG TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	CA	---			ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAACATCAGATGTACAGAACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAAT[C/A]CAATTTTCAGNAAACAAAAATCAAAAC ATTAAGNCCCTGNNATATTTCTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCTATTACCCAGTCTAGGGATTCTG
NIB551	161	CT	---			CGTCTTTCTTTTGGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTGACTTAGGAACCCCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTCT/JTGACCACATACATCGGGCCATTGGTTGATTTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGTC
S72904	51	GT	---			AGCATAGAAAGTGATTATATTTTAAATGGTTTTCAAGTGAAGTTCTTTTGT/JAATTTGTGAGTTC ATTCCTGGAAATCTTTTGTGATTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAAAACCACAAAGTGTGTAACCTCCCTCTCTGTCAATTGGTTGTCTTTAAATA TTGCAAAAGTCTGATGCTAACAGATTTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC CATTGAGATAAATGGCAGTACTTTAGGACACACACAAACACAGAC/TACACCTTTTGTATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCTTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTGGTGGACAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTTCACANTCAATACTGTTGAACAAGAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCTCACANGCTGTATTACCTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAAACAGTTTTCCTTTAATTGTAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCTCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAAGTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTTGTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	---	CCAGTTTGGCTTCTGTCTCCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	---	---	---	AGGACACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGGNGGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	---	CCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTTAAAGGC TTGCCCTGGTG
ESTC142	72	---	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAAGACGTAATACTATTTTATTCATTTTAAATC AAAGANACCATTCATTCCTAACAAACA
ESTC143	29	---	---	---	---	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCTTTTG
ESTC144	26	---	---	---	---	AAATCCATATTTCTTGACATGAGGTCGTTTTAGCAGCATTTCCGG
ESTC146	20	---	---	---	---	CATGTCAGGATAAGGAGCANACACAGGATTTATACAGGTGGCAGCG
ESTC148	42	---	---	---	---	TCITTTGGTTGTCTACACAGACACTTAAAGTACTGTATCGCTGTNATGCGGCGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGCTGAG
ESTC149	28	---	---	---	---	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCTGG
ESTC15	28	---	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGAICTT
ESTC150	20	---	---	---	---	CCAGGAAACAAAGCACACANACTTATAGAATCTTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	---	GAAGCTAAGGCCCCCATTTTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	---	TTTTTAATTGACAACCTCAATCTCTACATACATACAGTNTTGCACGAATTTAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTACA
ESTC156	32	---	---	---	---	GCAGCATTTGTGACAGGAGCGCAAAACAAANCTGGCTGCCCTGGGATGGAGCGGGGGCGCTCA CCACCACTGCAT
ESTC158	35	---	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	---	AGCTGGCAAGAGACTTCTGAGGCACATCAGTACGTTGGTCAATTTAGGGCACGGTCTGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCAACCACAGGACAGGTT
ESTC160	38	---	---	---	---	TCTAGCATTGCTGGTGACGTGGGGCCTGAGCTGGGNGCAGTGGCAGTGTCTACTGGGCCCCGTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	---	CTCTCGTCGGTTTGAAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAATATTGGTTTGTACANCAGAAATACAATCCAATATATAACAATTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGTCTGGATTAGAGGAAAGTGCCCGCTCTGTTTCCATGACTT
ESTC176	23	---	---	---	---	CACCTCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAATTTTNCCTTTATTCTATTTAAATACCTTTTAT TCTCTTTATTCCTCATAAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGCCGACATCAGCATTTGCTCTGTCNTGTACAGCTCCCTTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGNTTAAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCTTCAGCTTG ATTTTCAACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	---	---	---	TCTATTACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATACTCATCTTGCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGAGAAAGNACTCAGCATCAGCTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACCTTTCCCTTAACCTTATCAGTCTAGTAAGCNTTCAAAGGAGGAAAATGGGTTAG CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCCTCTCCNGCAAAGTCTCCACAAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGCGTATAGTAAGCTCTGNGGAACCTCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAATAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	---	TCTTACTTGGGTAGTTTAGCAACATTTTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGAGGGAGGACAGACGNCAGCGCCTGGGTGGCGCCGCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGOC
ESTC203	27	---	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGGATAANAGCAATACTATTGTTTAAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	---	CTCCAGAGTCCCTCCTCANACAGGGGAGGAGGTAGGGAAT
ESTC216	49	---	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTTAAATTAATCACAGGTATTNTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	---	TTTTGTCAAGTAATGAGCAATACACTGANTGGAAATCTGCATGATTAATAACATTAAACAAGTTTCAT AAACACACCCCA
ESTC219	32	---	---	---	---	GTACACATCCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAGGGAAGC
ESTC22	41	---	---	---	---	TCATTGAAGAAATTTATGGGTTTATTCTTATTCTTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCAAGTAGTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	---	---	---	---	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACA
ESTC225	20	---	---	---	---	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAAGAGCATAAGTGCTTCAGAAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	---	TTCTACTTTATTTCATATCCCACCACNATAACGACTCCTTTAATTTAAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	---	GCTTCCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	---	CAAAAGGGTAGTCATATTTCCCANCAACAGCATGATAAAAATAATTCAAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTCTTCCTCTATTCTCTATAAAAAATAAAGGAAGCAGAAATCTG
				---	GC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTATTTCTTGAGCCGCTTGTCAGGTTTGAT
				---	TGGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATAATNTCAGTCGGTGATCATTTGTAATATACAATAACAAAG
				---	CAATTTCCCTCAGA
ESTC33	25	---	---	---	AGCACTCCAGCTCCTTGACGTTGNGGAACAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAATCATTTATGCTGATGGAAGAAACCATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTTGAACNCTCTCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGTGAGCCCTGCCGTGTCCATGGGOCAGGGAGCCACTGGTGCGGANC CGGGCAGATG
				---	TTTACCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGGAAGGACACCA
				---	AGT
ESTC57	20	---	---	---	AAGTGGGCCCTCCAGTCCCNCTCTCTGGGCACAGATCCACAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATNGTCCAGACTTCAGGAAAAATGATTTCC
				---	ACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNITTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATG
				---	TGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTTGGCTAGGCGTGTCTCATCTGTGAATTCACAGCGCAATGACAGCANCTCTCTCCC
				---	ACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGGCCCCACGGGAGGCTCGGGGAGACGACACTTTTCCCTGGGAAA
				---	GGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGANACCCTCAAGTTTAATCCCCACACTTACTTACTGCTCATCCGT
				---	CACITTCGCTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGGCTGTGGGCCAGATAGCTGTTCTGAGTTGCANGCAGCATGGAGATTGGACACT
				---	G

ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGGNTTTGGGGTGACGCCTAAAAAGTGTGACC AACAAATTCACAGCTACAGGAAATCTAGAACAAAATCAATATTCATCACNTTGGGTTGAAAAAGTTG GAAGA ATGACTTCTCTGCCATCGGAAACAGAGTTTCCCAGGNGAGCCCTTCTCTATCTGCGGTTA
ESTC74	49	---	---	---	GGCTCAGCACAGGGATAAGANCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGGTCTGAGATGINTCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC77	40	---	---	---	CAAAATCAAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAAACCT
ESTC81	20	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGTGTTGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC82	25	---	---	---	ATTGCAAGGAAGTGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC83	53	---	---	---	CTGGTTCCTTCGTCCTGGCATTCGTCCTCTCCTCNGGCCAGTGCTCCACCCAAGTGTCTCCCGATGAT
ESTC85	28	---	---	---	CTCCCCCTCTCAGTTTCACAGTGGAGACTANGGAGATTTCAGGGCAGGATCC
ESTC89	22	---	---	---	GCACGTTCTTTGTTCTCTCTCCAGAAGTGACGCTCTATTTAGTTGATTATCTGTCG
ESTC90	33	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTC GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTCTTGACTGTCTTCCA[CT]GCCAG ATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAAATCAAAAGAAGAAAGGCTTAGCTG
ESTC93	29	---	---	---	TTCCATCTAGATATCTACTCAAATAATTGAGACAAGTTTCAAACAGAAAGACGCTTGCTGTA TGTTTCATGGC[A/G]GCCCTATTACAGTAGCCAAACGATGAAAAACAACCCCAAGCTATATATACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGATCCCTACTACTACTGTGGAT
ESTC95	32	---	---	---	CAAATACCTGGACTATCAACCTTGTTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCACAGCGTGCCACCCAATCATGCCAGCTTCTGTATATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGGTATCTGGGAAACCAAGCCCTATCTGAGTCTTGGCTTCTGCTCC
DWU-100	127	CT	---	---	
DWU-177	77	A G	---	---	
DWU-286	213	A C	---	---	

DWU-252	94 A G ---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTACAAGGCACCTTCATGTAAAGTGT CAGAAAGGAGCTACAAAACCTACCCCTCA/GJTGAGCATGGTACTTGGCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCTGTTGAATGACAAAGTATGTGGTTTGTGA
DWU-330	85 C T ---	---	AT GAACATTCCTCTGCAGCACTTCACTACCAATGAGCAATTAGCTACTTTTCAGAAATTGAAGGAGAAAA TGCATTATGTGGACTGAA[C/T]CGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTCCCTTTTGCAA CAAGACAAAGCAAAAGCCACATTTTGCAATTAGACAGATGACGGCTGCTCGAAGAACAATGTCAAGAAA CTCGATGAATGTGTTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	GAAATGTTAATTGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTTGGTTTTAAAGAG AAGCATCATTTCCCAACAGGGCAACTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAAAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCCCTA/GJGCATCTATTTCCCTCTGTGC
DWU-1537b	89 A G ---	---	CTCTTAACTTCAAGTTCCCTCATCTATAAGAATAAGGGATTCAGTTGTGATCACATAGCTCAGGTAATC CAGGACAGAAAACCCAGGAGC/GJTGGAACCTGATCCACAGCTAGAGGATGGGGGACTCTGTAGCT ACAGCATTTTCCGTGAACACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	CTCTTAACTTCAAGTTCCCTCATCTATAAGAATAAGGGATTCAGTTGTGATCA/CJTATAGCTCAGGTA ATCCAGGACAGAAACCCAGGAGCATGGACCTGATCCACAGCTAGAGGATGGGGGACTCTGTAGCT ACAGCATTTTCCGTGAACACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	ACCATCTTATAGTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGCCCTGGGGAATTCAGGTCAGTGTCTCTCTCTCCCTGTCCTGTCGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGCCCTCGGCACTGAGCTG[C/G]AGA CCCGCAGACCAACTCTGAGCTTTCTGGGCCCTCTGAGTCTTGTCCTC
ESTD-ADAA	184 G A ---	---	ACCATCTTATAGTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGCCCTGGGGAATTCAGGTCAGTGTCTCTCTCTCTCCCTGTCGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGCCCTG[G]AGCACTGAGCTGCAGA CCCGCAGACCAACTCTGAGCTTTCTGGGCCCTCTGAGTCTTGTCCTC
ESTD-ANT1	160 T C ---	---	TCTCCTGTCAATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGGCAATTAACCAAGTAATTCA TGGACTGCCCAACTCGAAACAAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGGGGTTACCTT TTTTTATGGAGGACCGAACTGAGGCT/CJGAGCTCAGATGATCCTGT
EST10398 2b	188 A G ---	---	TGCCTGGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCAACCCTTATCTACTTGTATGATGTTTCACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTTGTTTCTTCGGGCCAAGAAGGTATCTACCC/GJATAGTGTCTATTAGGCATTTTG

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EST10398 2a	147 C T ---			TGCCTGGGTGGCAAGGCTGCAACAAGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGOCACCTCTTATCTACTTGTATGATGTTACACATTTGGGGCTTGACTTTCCACACGGGAGAAAG CAITGTTTCTTCTGCTGGGCCAAGAAGGTACTACCAATAGTGTCTATTAGGCATTGG
ESTD-C7	14 G C ---			ATATCGTGGCCTTA/GCTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---			CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACCTTCAAGG ATAATGGGGCAATCACTTCTTTTTCCTTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ---			AGTCTTCATCTGGGGTGTCCAGGTAGATCCCTTTACCG[G/A]CCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---			CTGGGCTGCGCCGACAGCTGCTGGCACCTGGACGGCGGGCCAGGCTCACCTCTATAGTGGGTCG TATTCGTCCACAA[G/G]TGCACTCTGGATCAGCT
ESTD- HRASa	37 C T ---			CTGGGCTGCGCCGACAGCTGCTGGCACCTGGACGG[G/C]TGGCGCCAGGCTCACTCTATAGTGGGG TCGTATCGTCCACAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---			GGAGGACAGGAGTGGGGAGGGGTCTGCTCTCCAGGTCCACAGACCAGAGAAGGGGCTCAGTG TATCCCCACCCCA[G/G]TGGGGCTGGAGATGAAGAGGATGATGCAGGT
ESTD-OTC	18 A G ---			GTGACCTTCTCACCTTAA/GA/AACCTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAACAGAAAGGAGGATGTAAACA
EST36751 7	36 C T ---			CCAGTGTGTTCAAATTTAGCTTTGCAGGTTTAACTC[G/T]GATTACTTTTCTATTCAAATCTCTGTGA AAATTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109 A G ---			CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAGTTTCTACTGGATGCATTAATAACAAAT[G/G]TTTACCTTTTGAAAAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAAGAGTATCCGTACCGTCTGACGTTTTGAAACAATACA GATGCTTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCTA
EST18288 3	121 C T ---			GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA[C/T]GGGAGCCAGT GTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGGCAAACTCTCTGCTGGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT[C/T]TACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180 A G ---			AATCCAGCACCTTAGGAGGCTGAGGCGGATATCACAGAGGTGAGGAGTTTGAGACCAAGTCTGA CCAACATGGTGAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGATGGTGGTGCATGCTGT AATCCAGGAGGCTGAGGAGGAGAAATGCTTTGAACCTGGGAGGCG[G/G]AGGTTGTTGGTGAGCCGA GATGGCACCATTTGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGCTCTC

EST70523 3	182 GT ---			TTCCGGCCAGCCCCCATCTTGGCACCCCTGGTCCCTCAGGGGCCACCCGGGGCACTCACCGCTCT CGCTCTGGTAACATCCGGCCGGCGGCTCTTGGACACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCGGGCTTGGCAGGGCCAGCCCTG/TGAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACAGTG
ESTD- APOA2	101 CT ---			CCAGGTGTGTGGCACGTGCCTGTATATCCAGCTACTCGGGAGACTAGGCGATGAGAACTCTTTGAAC CGGGAGGGCGGAGGTTGCAGTGAGCTGACATGCTG/TGCCACTGCACTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 CT ---			CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTGAGCATCTTTGGCTCACATGAAGGCCAAATCCGAGAGAGC/TCTAGAAGATACACGAGAC CGAATGTATCAAAATGGACATTGAGAGAACTTCAACGATACCTGTCTGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGACTCTTGCTGCTAAGAACCTT
EST74167 6	137 C ---			AGACATGAAGGAGTTGAAGGCTTACAAATCGGAATGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCGCAGGCCGCTGGGCGGGACATGGAGGA CGTGGCGGCGGCTGTGTGAGTACCGCGGCGAGGTGCAGGCCATGCTGGCCAGAGCACCGGAGGAGC TGCGGCTGGGCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8	132 C ---			CGCTGTGTGAGTACCGGCGAGGTGCAGGCTATGCTGGCCAGAGCACCGAGGAGCTGCGGGTGCG CCTCGCTCCACCTGCGCAAGCTGCTGAAGCGGCTCTCCGGATGCCGATGACGTGCAGAGCGCC TGCGAGTGTACAGGCGGCGGCGCGAGGCGCGGAGCGGCTCAGCGCCATCCGCGAGCGGCTG GGGCGCTGTGTGAACAGGCGCGCTGCGGCGCGCCTGCTG
ESTD- ARSB	126 A ---			GGAGAAATGGAGCTGTGGAGGAGGCGCTCCGAGGGTGGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAGGGGTGAAGAACCGGGAGCTCATCCACATCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACCAATGGCACAAAGCTCTGGATGGCTTGACGTGTGGAAACCATCAGTGAA GGAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATGACCCAAAC
EST36770 4	144 C ---			TGTAGCCAAAGTCACTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACTGGTTTCCCTTCTCTTCTGATCAT TCTTACAAGTTATACCTTATTGGAGGCGCTTAAGAAGGCTTATG
EST26021 1	137 A ---			TAATGTAGCTCATCCACCAAGAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAAAATGA GCATTAGCTACTTTTCAAGATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTCTTTTGAACAAGACAAAGCAAGGCC
ESTD- BA511	29 A/G ---			GGGCAACATAGTGAACCCCATCTCTACATG/AAATACAAAATAGCCAGGTGTGGTAGCAAG TGCTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCTGGGAGGTGGAGGCTG CAGTGACCAAGATGGTCCACTGCA

ESTD-BC12	116 A G ---			AGCTGGATTATAACTCCTCTTCTCTGGGGCCGCTGGGGTGGGAGCTGGGGCGAGAGGTGCCGTTGGCCCCGTTGCTTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAAC/A/GGGGTACGACAACCGGGAGATAGTGAAGTACATCCATTATAAGCTGTCGAGAGGGGCTACGAGTGGGATCGGGGAGATGTGGCGCGCGCCCCCGGGGGCGCCCCCGCACCGGCGCATCTCTCTCTCCCA
ESTD-BCR	69 C T ---			CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGA/GA/CTJCAAGAGGTCAAGTCTCTGTGTCCCGGAAAGGGAGGCAGGTGACAAGCTAACTCTGCTTCAAAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCTGGCACA
ESTD-BRCA1aa	119 C T ---			AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTATAAGTGGAGAAAGGGTTTTGCAAACTGAAAGATCTGTAGAGTAGCAGTATTCA/C/TJGGTACCTGGTACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAACA/GAACCAATAAAT
ESTD-BRCA1bb	139 A G ---			ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAAACATTCCAAGTACAGTGAGCAACAATTAGCCGTAATAACATTAGAGAAAAATGTTTAAAG/GAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA/GTATTAATGA
ESTD-BRCA1cc	126 A G ---			ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAGGAAGATAC/TAGTTTTGCTGAAATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAGCGTCCAGAA/GJAGGA/GAGCTTAGCAGGAGTCTAGCCCTTACCCATACACATTTGGCTCAGGTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTGAAGATGAAGAGCTTCCC
EST512120	122 A C ---			ATCCTGAGCTCGCCAATAAGCTTCTTGTTTCTACTTCTCTCTCCACAAGCCCCCAATTTCACTTTCTCA/GAGGAAATCCCAAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACA/A/CJAAAGGCCCTCTCTACATCT
ESTD-C1R	40 A G ---			ACACAGGTGCTGGCACTGGGCTGGGGATCCTCTCCCTJAGJATTTGCTCCGGGAAGCACATTCAATCAA
ESTD-C1R	40 A G ---			ACACAGGTGCTGGCACTGGGCTGGGGATCCTCTCCCTJAGJATTTGCTCCGGGAAGCACATTCAATCAA
ESTD-C6	31 A C ---			CCCAGTCAGTTTGGGGACAGCCATGCACTG/A/CJGCCCTCTGGTAGCCTTTCAACCATGCATTCCATCTAAGCTCTGCAAAAT
EST201182	119 C ---			GTCCGAATCCTCCTCTGAAAGTGGCCGGTTTTAATCTGCTCATGACGCTGGCGCTGTGGTCCAGCTGAGGTAGGGGCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGGTCTCTCGTGCACTCCTAAGCTCTGAGAGCAAAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTCTGCGTGCATCCTAAGCTCTGAGA
EST530186	67 A G ---			ACAATCCAGGTACACATTCAGAAAGAGGGGGTGGTCAAGTGAAGCTGGGTAGGTCCAGTAATCCA/JAGJGGATTGAGGAAGGAGGCCACAGGATCGAAGTTAGTGAAGTC

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ESTD- CB22	119 C T ---	---	GGCAAGTTTTATTGATAGAGAGGAATCAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGGAGTGCCAAACCCATAGGGCTGGATACAAAAG ACAGGCAAGGAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGGCCCTACAGGACCAGACAGCT CTCAGAGAACCTAGCCCAATTACCTTCCCTTCCAGAGGACCTGAAAACGTGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAAA
ESTD- CB24	145 A ---	---	ACCAGGACAGACAGCTCTCAGAGCAACCTAGCCCAATTACCTTCCCTTCCAGAGGACCTGAA AAAGTGTCCCAACCCAGGTCGCTGTGTTGAGCCATCAGAAGCAGATCTCCACACCCCAAG GCCACACTGGTATGCCCTGGCCACAGGCTTCTACCCGACACAGTGGAGCTGAGCTGGTGGGTGAATGG GAAGGAGGTGCACAGTGGGTGACACAGACACCCGACGCCCCCAAGGAG
ESTD- CB25	146 A G ---	---	GTTTCTTTCAGACTGTGGCTTACCTCCGGTAAGTGAAGTCTCTCTTCTCTCTATCTTCGCCGTC TCTGCTCTGAAACAGGGCATGGAGATCCACGGACACAGGGGTGAGGAGGCCAGAGCCACCTG TGCACAGGTGAGCTACATGCTCTGTTCTGTCACAGAGTCTTACCAGCAAGGGTCTCTGCTGCC ACCATCTCTATGAGATCTTCTAGGGAAGGCCACCTTGTATGCGGTG
ESTD- CB27	125 C T ---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTGCATTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGACQCTTATCTTTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCTGTTTCATCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	TTTTCTGTTACCTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATATGTA TTTCTTAAACAATAAACTTGAAAGTCCAAAATTACTCTTGATCCATGGACTGCAGAAATAAATGTTA TTTAGCTGTCAGAAAAACAATACTAATCTTGACATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATAATTTGAGAGGAATCTTGTTCATGCAATGCAGTAG
ESTD- CYP2D6	61 A G ---	---	CAGGCCAGCGTGTGAGGTGGTCAACCATCCCGGCAGAGAACAGGTGACGCCACTATGGCA/GJCA GGTTCATCATTTGAAGCTGCTCTCAGGGTTCCCTTGGCTGAGCAGGGCGGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---	---	AAAAAACAATTTAACACCTTTTCAATCATATACACCAATA/CJATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTACTTGCAATCTAAAATGTCAATACTGATTAATGCAAGTTCAACAG ACAACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---	---	CATCCCCAAGCCCATCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGCGGTG GGGTGTGGCTATGTGGTGTGTGTAGTGTGGGGCTTTGGTTTCAGTTGCACTATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCTC

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ESTD- D17S33a	75 CT ---	---	CATCCCCAAGCCCATCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGTC/JACACATCAGGGGGCCCTACCTTTGTAGTCATGGAAAGGCTCTCTGGGGCG GTGGGTTGTGGCTATGTGGTGTCTGTGTAGACGGGGCTTGTTCAGTTGCACTATTGCGTT ATTGAGATTGCTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCCCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCCATGCTATGTAATCCAGCTACATCGGGAGGCTGAGGAGGAGAAATTGCTTGAACCCJA /JGGGAGGAGAGCTTGCAGTGAGCCCAAGATCACACCACTGCACCTTACAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD- D3S11	44 G ---	---	AATGATTAGAACCTGAAATACATAATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTCATCATTAATAAATCCATAAAGTACACTGTAAATAAGAAATTTAACAGAAATATCATTTGT TTATCAAACCTATTATCACATTAATTTATTGTTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCJA/GGGAGCCTTGATGTCATTCTGTATCTCCT CAGGTATCCACCTTGAGAGCTACTTTTCAAAAACCTCTACAGCCGTTGTTTATTAAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 CT ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAACATACACTGCTCTAGAACCCAGAGTCATAGTGTCTGTTCGGTCTTACGATGG CAGGTATGAAATATAATACTGTCTCTTTATTGGAAAGGATGCJCTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAACATACACTGCTCTAGAACCCAGAGTCATAGTGTCTGTTCGGTCTTACGATGG CAGGTATGAAATATAATACTGTCTCTTTATTGGAAAGGATGCCGGTATGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAAATGTATAATCCTGAAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJAGJGTCTCTCTACATCATCTTTCACAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTGGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGTGGGAGGGAGACA GAATGCTGATTJAJCTGTGGTGAACCAAGAACTTCTGGCTGTGGGTAGGGGAGCTGCTTCCAAAG ACCTCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DMa	66 C G ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTGGGCTCCACJ GJTCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGTGGGAGGGAGAGA CAGATGCTGATTATCTGTGGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGAGCTGCTTCCAAAGA CCTCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT

ESTD- DRD1	154 C T	---	---	TCCCAGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATGCCAACCCATCAC ACAAACGGTCAGCACCCCACTGAACCTGCAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGIC/TTTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144 C	---	---	TCTGCCTTTGGTCAGGAGGCTGCCGGGAGCCAGGAGCTGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCAGCCACACAGCTGACTCTCCCGACCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCGACAGCCGCAACCCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T	---	---	AAGACGATGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTGAGGTGGC/TTACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCTGTGAGGAGA
ESTD- ERBB2	93 C T	---	---	TCTTCAGGATCCGCATCTGGCGCTGGTTGGGCATCGCTCCGCTAGGTGTACGGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCACTGTC/TTGGGGCCGGTGCAGACCCACGCGGGCTGGGAGGACTTCA CCCCGCTCACCTCCGTTTCTGCAGCAGTCTCCGCATCGTGACT
ESTD- ETS2	43 A G	---	---	ACTCACAGTCTTTAAGTGAAATGGTGCAGAAAGAGGACCC/AG/GGAAGCCGCTCCTGGCGCCTG GCAGTCCGTGGGACGGGATGTTCTGGCTGTTTGGATTTCTCAAGGAGCGAGCATGTCTGGACACA CACAGACTATTTTAGATTTCTTTTGCCTTTTGAACACGGAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTCAGAAATTAGTTG
ESTD-F9	111 A G	---	---	AGATCCTGATGATTTTTTCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTGTGTAAAGTATGATGTTT/AG/GTCAAACTTCATTTTTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAACAAAAAC
EST68787 5	144 A	---	---	CTTCTATGGGATTTGACTTTATTTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAATTACACAAGAGGAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTTGGTGTACACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GDDH	200 C G	---	---	CGCAGACCGGTGAGTGGGGTCCGGAGTGTGGAGGGAAGGAGGGAAGTGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGGGCGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTCCGACCGTGTGTTCTGCTGCCCTGTTTACGCTGTCTGTGCTGCCGAGTTC/
ESTD-GCK	88 A G	---	---	GGACTCTGTCCCGGAATCCGAGAGCT GTTTATGTCATGGCAGCTCTAATGACAGGATGTCAGCCCTGCTGAGGCCACTCCTGTGTCACCATGAC AACCACAGGCCCTCTCAGGA/AG/CACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCAGCGCGCTGAGCCCCAGGGAAGCAGGGCTAGGATGTGAGAGACACAGTCT ACCTGCAGCCTAATTACTCAAAGCTGTCCCCAGGTACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGGCCACAAAGAGACCGGCTC/AT/
ESTD- GNAT2	56 A G ---	---	AGGATCCCAAGGCCCAACTCCCGAACCACCTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD-HT2	154 G ---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCCAC/AG/GGGCATCA TTGAAACCAAGTTTCGGTCAAGACTTGAAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT5	149 C ---	---	GGGCTAAATTTCCGAGCAACTTGCATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGCAGAGAGATAAAAGGATAACCTGGGTTTCTGTGGC TTTGCTTCTTACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAACGGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT5	149 C ---	---	AACACACAAGCCCCAGCGAGAAATTGAACCTCGCGACCCCTGGTTTACAAGACCAGTGCTCTAACCCCT GAGCTATGGAGCCCTCGTCTGTGTGGTTTCTTCTTTCATCTTATAGATTGATGTATGCTCCTA GCATTCGGCTACCGAATAGGATGTAGCTTGAGTAAATCCAGGATATTCTCTACAAAATGAAA ACATTTTCGTGCTGTAAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCCGTTGGA CTTTGAGTCAAAATTTGGCTGGACTTGAGTCCCTGACCAGCAAGAGAAAGAG/AG/CCCCAGA AATCAGGTGGGACGTCGGCTACCGCATCTCCCTTCTACGGGAATTTTCAGGGTAACT
ESTD- IGFBP1	43 C T ---	---	ACCCAGTGGAGCCCGCTCAITGCACGGTCTTGGCAGGAGTGCG/CTTGGGAGAGAAAGGAAGATG TTCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTTCAATGGATACAGAAATTTGGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCCTACATTGTGTGAGTGACGGGCGAGTGGGATCCGAGAGTGTGGGG TGCACGGACATAATGATTTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATTATTATTATTTATTTATTTTGTG AGATGGAGTCTGCTCTGTACCCAGGCTGGAGTGCGAGTGCG/AG/CAATCTCGGCTCACTGCAAGCT CTGCTCTCTGGGTTTCATGCCATTCTCTGCTCAGCTCCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAAATTTTGTATTTTGTAGTAGAGACGGAGTTACCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTCTCTGCTC/AG/IGGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGGTGGCTGGACCCAGGCCACGCTCTGCAGCAGGGAGGAGTGGCTGGCTCGTGAAGCATG TGGGGTGAOCCAGGGGCCCCAAGGAGGGCACTGGCTTACGCTGCTCAGCCCTGCTGCTGCTGCT/AG/ TCCAGATCACTGTCTCTGCGATGGCCCTGTGGAATGCGCTCTCTGCGCTGCTGCGGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGGC

EST45311 0	151 C T ---			GGCCTCCTCTTCCAATTCTGTGCCTATAGTTTTCTCTATTAAAGTGAACATACATGCATCTCTTTTAGT GGATAGATGCACACAAACACACAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAATTC/TACCTCTTTCAITTAACAGCCCTATTCAATGGCCTTTTCTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G ---			TGCCCATCAGCGGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCAACAAATTAACAGAAAT CCAGTTATTTTCGAGCCCTCAAAATGACAGCCATGGCGCGGGTCTCTCTGGGGCTCGTGGG GGGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTCTCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26 A T ---			ATGCAGGATGAAGGTGGACAGGGAGGATGAGGGCCAACTGTATCCACAGGCGCTGCAGATGTCG CTGGACTATGGGTTGTGACCCCACTGACCTCATGAGCATCAGGG
EST62782	149 G T ---			ATACTAGTACAAGTGGTAATTTTGATACATTACATAAATTATTAGCATTTGTTTAGCATTAACCTAA TTTTTTTCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTAAATGACAGTGGAAG TTTTTTTCTCTG/TJAGGTGCCAGTATCCAGAGTTTTGGTTTTTGAACCTAGCAATGCGCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCATGCA
ESTD- KRT10b	183 C T ---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTC/TJTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT10a	133 A G ---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCCTATTACTTCTA/A GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8b	231 C T ---			ACCTCAGCCCTCCCTTAGCC/TJGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCA/TJGTCAACATTGACACA
ESTD- KRT8a	21 C T ---			ACCTCAGCCCTCCCTTAGCC/TJGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGAATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCGCTCAGGTTTACCAGTCAACATTGACACA
EST75099 6	82 C T ---			CACTTGTGTGTAGATCTCTCAGTGGCGCCTCTACTGGGTTGACTCCAACTTCACTCCATCTCA AGCATCGATGTCAA/TJGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGGCCACC CCTTCTCTGGCCGCTCTTGAGGTGTGG

ESTD- LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAATTTGAACGTAGCAAAACTGCATTGGTATTAGA AAATAAAAAATTTCCAATATGTAGTGTCTGTATTACCTGCCTCTGCCATGCAGCATATAGCCTGT GGGAACCA/GJGGAGGGCTTCCCTTACCACCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGCGCAAATCTGACACGTGTGCACCCAGGTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTGACJACAGATTCTCTGGAAGACAGCAGCGGGATGGGGGCGAGGAGAGCTGCCTGGATGA A
ESTD- LMP2	35 C G ---	---	TACACACTTTCTTACCCATTCACTGAAAAAGACTC/GJGCAAACTGGAGCCTTTGTAGGAATGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTTCAGCTTGGCCTGTCTGCTGCCTGCA AGGGTTTGTCTAATTCATTCATGCTCTTCATCTTTTAGTC/TJAGCTGTGGGTTTGTGTTGTG TTCTCTGTTTGTCTAGTATCTGACTACTTTTAAATATAAAAGAGATGTATCTAAACAAAAATAG AGATTGTTATCAGAAGTTCACAACATTTATAAAAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCCTCCCAAGCTGTCTCCCTAGCTC/TGAACCTCAGGACAACGTGC AG
ESTD- METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTCCAAAGGTTTGGTGAAGTTGCTGATTACC/C/TJGGATTTTCTGACG ATCTTCAACTGCTAGAGCACTGTGTTCTCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAACCTAGTACCAGATCCCACAGACTGATATGGCTGGT
ESTD- NFKB1	107 A G ---	---	AACATGGACTGTATATTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAAAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCTT/GJGCCCCAAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTGTAGGGACGAGAAAGATCATTTGAAATCT GAGAAAACCTCTTTTAAACCTCACCTTTGTGGGGTTTGTGGAGAGGTTATCA
ESTD- NPPA	45 A G ---	---	TGTCCTTAGGCCACGCCCTGCTTGTCTCCCTGGCTGTTATCTTC/TAG/GTACTGCAAGAGAACACA GACAT
ESTD- NPAS	202 C T ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATCTTTTGTGTTGATTATATATAGCAATTTGAGGG ACAAACCAGATAGCAGAAATGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTG/ C/TATCCCTGTGTTTAAATAAAAT
ESTD-PAI1	100 A G ---	---	GCCACCACACCCACCCAGCACACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGTCTGGACACGTGGGG/GJGTCAGCCCGTGTATCATCGGAGCGGCCGGG CACATGGCAGGGATGAGGGAAAGACCAAGAGTCTCTGTGTTGGGCCCAAGTCTCCTAGACAGACAAAAAC TAGACAATCACGTGGCTGGCT

ESTD-PAR	120 A	---	---	CTCTTCAGGAACCAACGAGTCTTACCAAAACACGACTTATTGCTGTCGAGAGGTACAACCCGCTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACCTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTTCACCTTTCTGTGTTCTAGAACGTTTTTCTAG GACTGGCAGTTTAAAGCTTTCACCTAGGCTTCTGTATACCCATGCC
ESTD- Per/RDS	74 A G	---	---	ACCTACAGACGTCGCTGGATGGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGAGGCGCTGGCTG CTGGAGA/GGAGCGTGCCGGAGACCTGGAAGGCT
EST68308	29 C T	---	---	GGAAAGAGATTTAAGAAGCTTGAATTTGGA/C/TAATCTGGTCTTTGAGTGTGGAAGAGTTTCATGTC TCTGCCTGAGTTACAACAGAACTCTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA
EST54045	39 A G	---	---	GGAAATTTAAAATATTTAAAATACCTCCATTTGCT/TA/GTCTTTTAGTGAAGATGATACCTGC AAAAGACATGGCTAAAGTTATGATGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAATGTTGACTTTATCAT
ESTD- PXMP1	88 A G	---	---	ATGAAACATGGTCTTTAAATTTATGATATGTTTGTATAGCTATCTTAAAAGGGCTTCTTTTTTTTA ATGAGAAAAGAGGGGAAAAG/GAGCGAGCTGTGGTGGACAAGGTGTTTCTCAAGGCTCATAC AGATTTTGAAATCATGTGTCCTTAGAACATTTTGTAAAGAGGTAAAGTCTTATGAAATTAATCTT
ESTD-RDS	127 A	---	---	CCCGAGGAATCTGAGAGCGAGAGCGGGCTGGCTGGGAGAAGAGCGTGCCGGAGACCTTGAAGG CCTTCTGGAGAGTGTGAAGAGCTGGGCAAGGGCAACAGGTGGAAAGCGGAGGCGCAGACGCGAGG CCAGGCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACCT CCAAAGACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- s14544	94 G T	---	---	TTGGGAAGTTAGAGCCTATATTTAAATACGGAATTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTG/C/CTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	45 A C	---	---	ATCACAGGTCTCTGGTCTCTGGCATCATTTCTCTGGGAGAGATGG/C/CTGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST19590	55 C T	---	---	AGGAGAAGCTGAGGAGGGGAAGAGACAAAGAAATGACATTTGATGAGTGAAGATGTC/TTGGCTCAG GATGCCGGAAATGAC
EST76136	39 C T	---	---	TGAAGCTTCTGCCACGCTTGCAATTTGTTCTTAGGAGAAC/C/CTGCGTCATACCTTTATCTATAGCCTT CCCCTAGGTCCT
ESTD- SPTB	176 C T	---	---	TGAAACACCTGTGTGTCGGAGCAGGTGTGTTTCTCTGGGAGCCTGAGGAGTTTGTGTCTGTGTG CAGTCCCCCGGCCACCTGCTGTTGAGCCTGGACATACACCTTCACTCTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCTGCGCTGTTGTGACAC/C/CTCTCTGTGAAGACCCCAACCCCTGC CTCCCCACCCAAAGCCAGTTTCTTAGCAAGGGCAGGAC

ESTD-TAT	224 C ---	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTTCATCAGGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGGACAGGATCA ATTCTCTCACCAGTAAACGTTTGTACAACTTTCTCCAGTATGGATGGGATATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THFB	125 A C ---	---	---	TGCGGCCTTTCTCCGGCAGGGTAGACTTCTTACTGGCTGTTGATTTCCAAAGAAAGAGTCCCAAG CACACGAAACAGAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATC/A/C/TTCAT CCACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCCTGTCAGCTTCTGGAATTTCTGCCACCCGCAACAAGAAGTCTATGC CAAGGCAGAAAAGCTGGTCTCATGGGCAAAATCAATGTCCTCCAGATTTCA/G/TATCCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCAATAATTTGATGTCGTAA CATGGGTGTGATCCATTTTCAITTTGGCCATAGTCCCTATGGGGATGACA
ESTD-TYR	122 G T ---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACITTTATTACCTTCTTCT AATACAAGCATATGTTAG/C/ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACITTTATTACCTTCTTCT AATACAAGCATATGTTAG/C/ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCAAGAGACAGGAAACACAGTG ACTCTGAGATGTCA/C/T/CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T ---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCAAGAGACAGGAAACACAGTG ACTCTGAGATGTCA/C/T/CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC/A/G/TGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCAAGAGACAGGAAACACCA GTGACTCTGAGATGTCAAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC/A/G/TGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCAAGAGACAGGAAACACCA GTGACTCTGAGATGTCAAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---			CTCTGGATGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCTACTGGAGAACAAAGGACAGCCAC/A/GTGGCGGGGATGGCCGGGGAGTTTC TGTTGCGGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGCGGTGCGATGCCTAAACCTTTGT TTCTTGGCCAAAGGAGGGGGGTGCCATGCTGAGATGTAGATGGGOC
ESTD-VWF 6	36 G ---			AGGTAGGAAAGCAAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTGG TCCCCTAGAGTCTG
EST71770 6	189 C G ---			AGCACCACTCTCAGTCAAGCCTCAGCACCATGCTGTTCTTATAAGGATGACGTGCTGTTTACAA CATCTCTCCATGAAGACACAGAGATTATTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGACTGTGATTGTGAACAACAAGAGAAACCACCTGCAGATCCAGC/GTGTGGTGGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
ESTD- TNFab	152 A G ---			TTCTGCATCCTGCTGGAAGTTAGAAAGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGTTTGGGGGCATGAGGACGGGTTTCAAGCTCCAGGTCTTACACACAAATCAGTCAGTG GCCAGAAGACCCCTC/A/GJAATCGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATG CTGTGTGCCCAACTTCCAAATCCCCGCCGCCGCGATGG
ESTD- TNFaa	88 A ---			TTCTGCATCCTGCTGGAAGTTAGAAAGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGTTTGGGGGCATGAGGACGGGTTTCAAGCTCCAGGTCTTACACACAAATCAGTCAGTG GCCAGAAGACCCCTCAGATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGCCCAACTTCCAAATCCCCGCCGCCGCGATGG
EST52418 6	113 A G ---			CAAAATACAGGGTCAACTGCTATGATGTTTGGAGCCAGTCACCTTTTGGTGGCTACAAGATGTG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTCAGGCATACACT/A/GJAAGTGAAAACTGTGAGTG TGG
EST13586 3	89 A G ---			CCCACTCTATTTGCCAGCCCCAGGACAGAGCTGATCTTGAACCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC/A/GJGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGTGGCTCCTGCTGCTGOC CCGGTCACTC
EST51976 7	123 A T ---			AGGCAGAACTGGGCCCCATGCGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCTTCTTCAAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG/A/TCTCTCTC CCTCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGGAGGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGG
EST11458 6	140 A G ---			CCACTTTGGTAGTGCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTTGTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCAATTTCCACAGTGGT CCC/A/GJTAAACAATTCTATGAGCCAGGAGAGATACGTATTCCTGCAAGCCGGGCTATGTG TCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGOC

ESTD- AT3aa	60	CT	---		AGACCTCAGTTTCTCTCTGTAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGC[CT]AGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGGACCAAGTGGAGAGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	106	CG	---		CGGTCTTCCTCCAGGTAATTGTCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCTAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTA[CTG]GTACAGAAAGGAGATGCATGAACA GCAGGAACACGTTGGAAGAGGCTGTTTCCAGTGTAAAGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112	AG	---		ACCTGGTGTGCTGGTGGTGAACCTGGTCTCTTGCCATTGCCGGCCCTCTCGGGGCCCGCTGG TCTCTGCTGGTGGTGGTAGTCTGGAGTCAACGGTCTCT[CTG]GTGAAGCTGGTCTGATGGCA ACCTGGGAACGATGGTCCCGCAGTGGTCAACCGGACACAAAGGAGAGCGCGGTTAACC TGGCAATAT
EST36027 2	120	AC	---		AGTGACTTCCAAGAAATGGCTACCAACTTGCCTTCATGCGCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTTGCATACATGGATGAGGAGACTGG[CT]AACCTGAAAA AGGCTGTCAATCTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGCAACAGCAGGTTCACTTAC ACTGTTCTTGATAGTGGCTGCTCTAAAAAGACAAATGAATGGGGAAGACAA
ESTD- COL2A1cc	112	AG	---		AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTGCTCACTTCT[CTG]GGGTGTTCAAGGTGAAAA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGTAAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97	CT	---		TGAGAAACACCTAGTCTCCATCTCTCTCAATGGGAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAACA[CT]TGGACTTCTTCTACTGCGAGGACAAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAACACTATCATGGAACA GCATT
ESTD- CPT2	150	AG	---		GCCGAATGCCCGGAGTTTCTCCAATGTGTGGAGAAGGCCCTAGAAGACATGTTTGATGCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGTACCATCACCTTCTCTCATCATGAAAAAC TGGGAGGCCGGCAT[CTG]GTGCTCATGCTGTAATCCAGCATTTTGAAGGCTGAGGCGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACT
EST12274 0	135	AG	---		CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTGCTTCCAAATAGAGCCCTTACCAAGTGTAT TACATAAAGAAAGTCAAGTGTGTTTACTCCTCATGACCAATACTTCTCCCTCTTAGGATGAGGTG[A/G]TAGTAAATGACCGATGGGTGTCAGAACTGTTCTGTCACCATGGAGGATACTATAACTGTGAAGA TAAATTCAGCCACAGAGCTTGCCAGATC
EST76807	91	G	---		ATGCTAAGGGGATCGGACATGAAGGACCTGTGAGCCGATTGCTCTATCTCCAGGGGCCCTGTCTATC CAGCTCACTCATCAATGGGCGCAGTCAAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	TTACATTTGTGGATTGTTTCTTTGCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGCTGTGGGATAATTTGAAAGAGATCTTTTGCCAGTCCCAATGTCCTAGA GAGTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCTTAGATTAAAGTCTTTAATCCATT TTGATTGATTCTGTA
ESTD-RVRI	109 A G ---	---	CTTGTGACGGGAGGTACGTCTCCGCTCTTTTCATGGACATATGGATGAGTGTGACCATTTTCCC CTGCTGACAGTATGACACGCGCAGACTTGCTACTATAGAGAGGGAGCTGTGTGCACTCATGCC CGCTCCCTCTGGAGGCTGGAGCCACTGAGAATCAGCTGGAGTGGAGCCACTGCGCTGGGGCCAGCC ACTCCAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTACCCGAGG
ESTD-WT1	70 A G ---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCTCCCTTCTCTTACTCTCTGCTGAGGATGTG CGAGJCGTGTGCTGGAGTAGOCCGACTCTTTGACGGTGGCATCTGAGACCAGTGAGAAACGCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C --- 62 C T ---	---	GATAAGTACACTGAGGCCCCAGGAGTTATTGCCTAGTAGCCCCACTGTGCATGCACGCTTAACCTCT GCACCAAATGGCTTCCAAGGCCGTAGGGAACTGGGGGATCTAGGGGATGGTGAGGAATGGCCC AGCCAGTCCGGCGGTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGACAGGAGATGGGC TGGATGAG
ESTD-PBDA	103 A G ---	---	GGAGCCAGGAGCGCTGCACCATGCCCGCATAGATCGGACCTCAAGCTCGACTTCAAGGAICTTG TCCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122 A G ---	---	CCCTTCATGCCAGATGGAAATCCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAGGGCAGGACTAATCCAAAGJCTCTACCCGAGCTTGCTCGCATACAG ACGGACAGTGTGGTGGCAACATTGAAGCCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	TGCAAAACACACAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGAGJTCAAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGAAACTTGAATGTTATTCAAC TGGATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-ACE	96 C T ---	---	ATGGCTTGCCTTGGATTCAGCGGCACAAAGGCTCAGCTGAACCTGGCTAGJCCAGGACCTGGCCCTG CACTCTCTGTTTTCTTCTTCATCCCTGTCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCGAGGCATCGCCAGCTTTGTGTGTGAGTATGCACTCTCCAGGCAAGCCAC GATCAAGCAGTGCACACGGGTACAGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCACTACAGGATCTGCGCTGTCTCCCTGCTGGGGGCCAACCCCGGCTTCCA TGAGGCCATTGGGACAGTGTGGCGCTCTCGGTCTCCACTCTGCAACATCTGCAACAAATCGGCTGC
EST54419 8	88 A G ---	---	CTTCTGCCTAATTGAATGATATTGTGCTGTGGGACCTGAGCACTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACJAGJATCCTGGGAGATGATTTGGGTTTAGCGTGGTCTGATGTGCTA CTATAGTCCAAGTGAA

ESTD-PS-1	99 A G ---			GGGAGTAAACTGGATTGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCATAGCCTAGTTCGTAGCCATATTAATTGGTTTGTGCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---			GGCTGCAGGGGTTCCGTGGAGGGCCCTAGCCGGGGCCCTGCTGGCGCTGGGGTCTGGCCACC GTGGAGGCAACCTGCTGGTCACTCGTGGCCATGCCCTGTTGGACTCCGAGACTCCAGACCATGACCAA CGTGTCTGTGACTTCTGCTGGCCGACGCCGACCTGTGTGATGGACTCTGCTGGTGGCCGCGGGGCCA CCTTGGGCGC
WI-567b	48 A G ---			TCTCAGACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTTGGTTCTGAGCCCTCATCTCTTTTA CAGGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGTCTCTTCTCCCAATCCATCTTCAAAAG GCTGCCACTGTGATCTTCCCAAGGTGATCTGTGATGCTACCATCTTGTCTTCAAGCC
WI-801c	58 G T ---			ATGGAACATTTCTTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTCTTCTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCAACAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---			ATGGAACATTTCTTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTCTTCTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCAACAGAGAGTTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---			GAAATTCACCTATACAAGAACTATTTCTCTAATTAATTACATTAGTCTCATTATCTGAAATATTAT TTTTACA/JGTACCCCTTGTATTTTGTATTCATTTGTAACGAGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTGTATCACAAATGTCTAAATACTTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTAAGGTTTA
WI-2529	71 C T ---			AGGAAATGGCTGATACCTCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA/C/TJCTTAACCTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---			TAAGGGCTGTCTTCCCCAGAGGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCTATGAGGTAACTTGAGGATGAAGGA GTGAGTCATATTGGTGGCAATTAATGAACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAGCAGCAAGGAGAGAAAGGAAGT

WI-2015b	190 A G ---			TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTTGCAGATAGCATGACCATGCTAGTGAACCCACACAGACTAT GTGTGAATCGTCTATTAGGGTTGCTATAAACTCTACATGGTGTCTTTCCAACTTAA/GJCATATACTT CTAATACCATAGAG
WI-754b	49 C T ---			GAAGGCACAGGAGAGAGATGGCTGTCATCTACCAGCCAGGAGAGAGC/TJACATTTATTGGTAA TCCATAAAGTGCATTCTTTAAAATTTGATTTACTTTAGA
WI-754	22 T C ---			GAAGGCACAGGAGAGAGATGGCTGTCATCTACCAGCCAGGAGAGAGAGC/TJACATTTATTGGTAA TCCATAAAGTGCATTCTTTAAAATTTGATTTACTTTAGA
WIR-1b	56 A G ---			AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAACTCTGATGATCGTACATCC/A/GJTGCGCTG GAGGGTGATGCCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56 A G ---			AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAACTCTGATGATCGTACATCC/A/GJTGCGCTG GAGGGTGATGCCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72 A G ---			TAAATTTAAAATGGGGCCAAATACACAGTACTTATCTCACAGCATTCTCTAAAGGCTAAATAAGAA GAAGTAA/GJCTAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGACTGATAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---			TAAATTTAAAATGGGGCCAAATACACAGTACTTATCTCACAGCATTCTCTAAAGGCTAAATAAGAA GAATGTATCTAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGACTGATAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---			GAGCCTTTCTAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209 C ---			CGGGACAGAGACAGAGAGAGAGTTCGTCAGCATTACAAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196 C ---			CGGGACAGAGACAGAGAGAGAGTTCGTCAGCATTACAAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194 C ---			CGGGACAGAGACAGAGAGAGAGTTCGTCAGCATTACAAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A ---			CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTACGTCCAG
WIR-5c	177 C ---			CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTACGTCCAG
WIR-5b	159 A ---			CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTT AGGTTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACAC AGTTTTACGTCCAG
WIR-5a	37 A G ---			CGGGACAGAGACAGAGAGAGTTCTGCAGCATTCA/GCAAGAGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTT AGGTTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACAC AGTTTTACGTCCAG
WIR-6	63 A C ---			TAACCTGAAACTTTGTCTTCTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[AC]
WIR-7	12 C T ---			CGCAGTCTGGGTTGGGCAG
WIR-8	46 C T ---			TTGCTGACTATTCTJAAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC GGCGTCTATGACTATCTGCTGGTCACTGATTGACTAATCTCTGCTGCTGGCCTTG
WIR-2	56 C G ---			AAACAGAAAAATAGAGGTTATAAGGATGGAACCTAAAGTTGTGAGAAAGAGGTATGA/GCTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATAACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WI-7069	93 G A ---			TGTCCTTGCTTATGCCTGCCTCTTTCGCTTGGCAGGATGATGCTGTCATTAGTATTTACAAAGTA GCTTCAGAGGGTAACCTAACAGAGT[G/A]TCAGATCTATCTTGTCATTCCTCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCAGTC
WI-18694	41 A T ---			GGTCATTTCCTTTTATCTGTCAGGAGCCAGCTGACTTJA/TCTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A G TGC	CCTATATTCA AGTTGGAAA	TTGTATTGCTG CTTGCAAT	CACACTGTTACACACCTATATTTCAAGTTTGGAAATGCA/GTATTTGCAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAAATTTATGAAAACATCCCT

WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTACCCCTCAACACCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA[C/T]GTGTGCACTGTCCAAACACAACCTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCAAAAA	GCTAAATTAAA CTGCACCTTTT GC	CGATTGACAACCTTTTATTTTCAACTTAGGTACAGTCCAAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAA[C/T]AGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGATATGTGGAAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T C A	GCTGTCACTCT AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT[C/G]CTCCGTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGTTCCTCCGA GGGTAC	TGAAGGCOCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGCACCAACACCAAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACCGGTTCTCCGAGGGGTAC[C/G]CCAGCAGGGCCTTCAAGCTTAAAGTCG
WI-18673	29	A G ---		---	TGTGGGCAAACTTGTATTTAATTGCAAAAC[C/G]ACTTAATTTACAGCACATTCAATATGAACCAAC AGGAGATTGCTGACTTTGTAAACATATGAATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GTGTTGGGGTG GGG	GCAAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTTATTTGGAGGTTAATCTTATAGGATATGAAAGGATTGAGCAACGATTGAGATT GTGTTCTCAGGAGGGCTCGGGCCAAAGTGTGGGGTGGGGGTGCAGAG[C/G]GTGCTCTCTTC AGTGGATTTCGGGACC
WI-18538b	91	T C ---		---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTTCATCCTAA[C/T]TACTGAAGCCATTTCTTTGGTTAACTTTAGA
WI-18538a	59	T G ---		---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAACTCCCGAGATTTCTTTGCTTTA TTTTATATTTTCATTTTTCATCCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C T T C	TCATCTGATAC CTTGTTGAGAT	AACCAGGATA AGGCTACAACT ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTGAGATTT[C/C]AAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAAACCTTT
D49493	159	A T T C T G G G A A T T			CAGGACTTGTGTGCACTGCAGACACAGACAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGGTCTTTCAATTGCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATTTA/TGGCCCTGGCCTGAAAGTGGGCCATCATTCATACCCACTGTT CT
EST10030	98	T C T C T C A A G T C C C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCTT[C/T]CATCCATACCACCACCTGCTGATTTG
EST10052	24	G A G A G G C T G		TGTGSAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG[A/G]AAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCTTC CTGTTGAGTCATAACCTGGTGGAGTGCATCATGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA A

EST10605 2	118 C G ---			CTTCGTAATCACAGTTCTGTATTCTATCATACAAAACCTTTGTTTCTCTGACAAAACCTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCCATGTG/GJTTGTGAGACTTAA AAAAAGAAAAGATCCC
EST11048 0	61 T G	CTCTCAAGTAG ATAAGAGGCA TAATCT	GCTAAATTTTC AGAAAGAAAT TTGTTT	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATATATCTT/GJAA ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTATTACACTGCAACCCAGAGAAGGAGCAC
EST11260 8	101 G T ---		---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAAGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATATCAATTAAGAATGAAG/GJGGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ---		---	TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCCACAGTAGATTCTTTGGACGAAGAAAATCCT TCTGTGGATTACGCTTACCGCCTTTCTCTCATCTGCTGGTG/GJTTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G TGGAGCCT	CCAACTACTT T	TCCAGCTTTCT CTAAAACTCC T	GAATCTGGGTATTAATAGCGGTGCCACAGGACACATAGGAAGAGCATCCAACTACTTTTGGAG CCCTA/GJAGGAGTTTTAGAGAAAGCTGGAGCCCCGAAGACCAGTAGTAGGAGTAGCCAGACCAA AAGGAGGAAGAGTGGAA
EST11772 6	74 A G ---		---	CCAGGAATAAAAGAAAAGATCAGAGGAAAAGAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA/GJGACTATTTCTGACTATAAGTGAATAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ---		---	CTTGTCATTTATTTTGTCATGTTGTTCTTAAAGGCTTGTAAGATAACTTGGAAATGTGGGAAC ACATAGATCCAGAG/GJATTAAAGGGCTGGAAGTAGCCTTAAGAC
WI-16644	42 G A TAC	CAATAAGCAG CTCATTTTGAT	ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGGATCTCAATAAGCAGCTCATTTTGATTAC/GJGGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAGCCTCCACAGAACTTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGAT
EST12005 9	56 A G CAAAGTCTGT	TTGTATAATA ACACTCAGTA	GGCTGGTCACT TOCTGGAT	GCCTAGTAATTCCAAAGGAACATGTTTGTATATAACACTCAGTACAAAAGTCTGT/GJATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAAATC
EST12055 9	32 T C ---		---	GTGGAAAATTTTATCTGTTACGCTTTCC/GJATTATATTATCTTGCTCTTGATTTCAGCACCC CACCCGATTTCAGGCAGTCTTTCTAACTGTGCCCTGTGAGCTGTTAAAAGTCTCT
EST12492 1b	95 A G ---		---	CCCTAGCAATGACTTGGAGTTGTGCCAATTACCAAGTTACATACTGTTGCCAAAATTAAAGCTCTC TCCCCAGAGGCATTAACTGAGATTAT/GJGGAAACGCACAGCAAAAATTGACGATGCAGCTTTTA CCTTTTA
EST12492 4	25 A G ---		---	ATCTTGAGGTTCTGGCCTGTCAG/GJAAAGTGACATCTTTTACTTACCACAGGTCAGGAACCTTAT AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTAAAGGGCTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAACCAAACTGGAGGCAAGTCCACAGGTCACACTTGTCAICIGCAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAATGCTACGGGGGAAATGACCAATTTTAAAGGGCCATGTG GTCGTGAGGCGAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAATTAGAATGTATCGGTAAGAATAAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATTATCCCAATGACAGTGTGCGTGAGATTCGATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTCTCTCTCTCATTTTATTGTTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGCJA /GJTGAGAATACAATATTGAAGAAGAGTCACTGCCTGCCCTTGGAATAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGGTCTCCAGGATCCAGICAJCTGTAGCTGTGTCATGAGGTCTCATCCATGCTCCACGG GTTCTGGGAGTGACCGGGATGGGAATCCATGTTGCTTTGCGTACTCCATCAGGTCATTGGC
EST12941 8	23 T A ---			TCTCAGCTCCACCTGACCTGCAIT/AJCAACAGCCCAAGTATTTTACCAGAAATTTGTTGCGTTTCA ATGTAGTGTTAGCTTAATACACTGCACCTGTTTG
EST12949 2a	52 A G A T A C T G T T	GGCTTTAATCA TAACCTAATA	TGTTGCTCCTGT GGTCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAACTGTTAAAAACAACACIA/GJTCGTCACTTG CAGAGACCCACAGGGACACACATCTCTCTCCTCCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTTAATGAAGCATAATAAACAGTTAAATCTGTTAAACCAACACIA/GJTCGTCACTTG GTGTAACCTCCCTAAATCAGTCTTCTAGGGCCACAC/CJGGAGCAGAAGCAGCTTCCCACCCAAAG CACCTCTGAAC
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTTTTAAAAATTTAATCGCTTTATACAATTGACACCAAAATAAAATGCACIA /GJATTTAAAGTTTACAATTTGAGAAGCTGACACGTTGCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTGTAGGTTTGTCTTCCIC/JAGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTTCTGTGTGTGCGAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAATAGTCT GGCCATTT/GJGACTAACCAAGTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAACATG
EST13230 6	72 G A A G A C G C	GCTCAGATGTG ACAGAGA	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTGGCGCTCAATATGCAGCTCAGATGTGAGAG ACGC/GJA/JCTCTGTACAGAGCCGGTACTGTCTTCAATCCTTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C T C T C A G G C C T	AACAGAGGGTT TGACAAAAGA	G	AAAGATATAAAACAACCTCCCATCAGTAGCAATACAAGGTTATACATTTTAAACAGATTTTCTCAGG CCTT/CJTTTTGGATACCCTTAGTAGTTAACTCTCTTTTGTCAAACCCCTCTTGTATATAACCA

EST13278 2a	51 A G G	CTTACCGAA CAATATTTAG	CATATCTGG GTGGTGAGAA	TTGCGAGAACGTTTACAAGCTCCAAACCTTTACCGAACAAATATTTTAGGAGAGATTTGAAATTAT TTCTGTAGTTCTACCAACCAAGAAATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTT AGTCCAAGA	GATGGAAAATT TGAGGAAGGT	GCTCACTAGATGAGCATGACCAAAATATTTAGATAATACCTGTTGGGAAAGTGCTGAAATTACTAGCC TGCCTGAGAAATCCACACACATTTACGTCCAAGAGATTAACCTTCTCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39 A G C T T	CAATTTT TAGA AGTTGGGTT	AAATCATTCA TGGAAATTTCA	AGCTCATCTGCAAGCAATTTT TAGAAGTTGGGTTCTTJAGJCTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATACATATTTTGT ATGTGGGGCTTTTGG
EST13518 2	45 C G ---		---	GAAACATCTCCAGTAGTATTGAGGTTAAATGATTGAGCATTTJGJACTTTTAAAAATTACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGATTG
EST13522 8a	66 A G ---		---	CAGGTTGGTGATTTCTCACTAGGAGCTATTTTGCCTCCATCCCGGCGAGTGCTGGAGACJ GJGTTTGTATTGTCACAACTGCGAGAGGTGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C ---		---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACTGGTTGAGAGCCATTGGTCTAGGAGTAGA AAJTCJGCACACAGGAATAAGGGAGAGGAGTTGCTGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G ---		---	AAGATTACGGACCATAAGAACTGCCCCCGACCCATACACACAAATTTATAGCAGGTAACCAAA CTGAAAGGAACAAAGTAATGACTTTCTTGAACAAACJGJTGATTACGAAAGTGAAGGGCTACAGGG TGATTACTA
EST14038 1	25 A G ---		---	CCTCAACCATCTGTAAACCGAGCCJAGJGAGTGACCGGACTTGCTGCTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGGTCAGTCAGCAGGTG
EST14083 7	23 A G ---		---	CAATGGTGTCATGTGAACATATJAGJACCTATTATCAATAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCCGAACAGGAGGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCAIT	GGAACAAGTC AAAATATTTT AAAAGA	AAATCAATGCAATCTTGTGGCATGCTAGACAGAGGCATTATTCJTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTCCCTTACACTCATTTTAAATGT
EST14812 2	50 A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCCTTTCAAGTCAGCTTCTACATTTCTGAATAJAGJGTACATAATGGG ATTTAAGTAAATCTTTAGAAAGTCCCGAGTTGCCCTTTCTAACATTTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T ATACTGGTT	CATCACCCAC ATACTGGTT	CGGGAACA GTACCGAA	TTTGCTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCGCTCTCCCGACTGAACCAAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAACTTGCCCGTCAACCCACCATACTGGTTJATJTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A ---				TTTAAACCCCAAGACCTTGTAGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTGTGTCATCATATATAGCCAAAGGACTC/AJGGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	GAAAGACAA AGACAACAGA	GGATAGCTGA AACAGAGATA TTATTCTC		GTCACAGCACCTTTTATTAAGACGTGAAAAGACAAAAGACACAGAGGA/G/CJAGCAGAGAAATAA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTA
WI-16739	57 G A CACAAGC	GGTTTGGCCAT GATAGTTGATG	TTCATTATTCC CTATAA		AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTGGCATCACAAAGC/G/AJTTATAG GGAAATGAACATCAACTATCTACAGCTAAACCTAATGAAGACCAAAATGGCTCCAAGGT
WI-16782	96 C T CACTGTAAGG TC	GGTGGGAGTCT CACTGTAAGG TC	CTTCTATCTTT CTGTTCTCTCA		CTTCTTCTCTCTAGACGTGGAAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGGA/C/TJGATGGAGGAACAGAAAGATAGAAAGTTTGGGGT GCTGATGAAATTTGGGG
WI-16783	64 A G G	TCCTGAGATGT CTTTACCTGA	CTGCTTGGTTC AATCCTTATTA	G	AAAAATGTAAACCTTAGAGGTGGCTCTTTTGTGTCACTTTTCTGTGAGATGTCTTTTACCTGAG/A/GJ CTAATAAGGATTGAACCAAGCAGTATTTTTTAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ---				CAGGACTTAAGGTCAATTTTGGCTGGGAAGACTTTAACTAAAGGTCAGGGCAACATAGGA/T/CJTGTA CAGCACCACTCGGACCAGGAAGTGTGAAAATGTGCACACTAGCGTGGCCAGGCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---				GGTTTGAAGACGCAGCTTATCTCCACCTGCCACTGGGATTCATTTTGTGAGAGCTGTTTGTGACGCC TTTTCCAGAAAAGGCCGCTC/G/CJGGGTTTCTGAACCCCTATATGGGCATTTTAGAAT
EST16089 9	96 C T ---				CGTCTGAAGTTTTCTTTATCAAGATCACAATCAATCCCTCGGGCCCCCTGCTCAAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC/TJAAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---				ATCCAGCTGTGAAGGGACAGGAG/C/GJGTAAACACAGTCCATTTATAAGGGGTGTGCACATTCCCA GGGGCTCCAAATAATGCAACATTTGTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---				TTCITTTAAATAACCCACAGACACCCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGTTCTCTCCAGGGA/JGTTTGGCCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---				ATGGTATAACAAAATCAGTTCAGGTTTTTTCTGGAACAAATGATCCTTTGGTCTTTCCCGTGGCATG CTCCTAAAACAACATAAACACCCCTCTACGTCTAATCAGTCACTTAAGATA/T/CJCGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---				ATGGTATAACAAAATCAGTTCAGGTTTTTTTTC/GJGTGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCTTAAACAACATAAACACCCCTCTACGTCTAATCAGTCACTTAAGATAATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ---			AGCCAAATCAAACGAACCTCTATCAAAACACACAAAGGCCCTAGAGGAGAGATTAC/TJAATGAACGT AAATAATTAAGGCAATTTTGTATCTAAAGCAATTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGTAGGGAAGATAGTAGTGCAATAAAATGGTAAACAGCAG/G/AJAATGGAA TTATAGCTTCTTTTCATATAGGAATTGAAATTTATTTACTGAGGGTGTAGGCAGAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAACCTGTGGTTACAGAGTATTGTTCTTTTCATAAAGAAAGAAATATCTAGTTG/A/GJGTAG AGGAAGGCACCTGTCTTCTGGCCCTTCTGTTTCATATTTTATGTCACTGTCTAAGCTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTCAAAATCA/G/ATACAGACAGATAAGAGCTTTAAGTATTTGCAATTT CCCCAGAGGAAAGTCAGCATCATAAACACATGGTCACATGCTCAGGCACATGGTGTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAG/T/CJCCCTGTGCAGCC CTTGCCAGTTTCCACAGGCGAGGATACTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACAGGCGAGGATACTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTCTTCACACCTCATGCTTGGCTGGAACCTGGTGCACATGTCATCTTGAACATATCATTTGGCAA AGGGAATGGGTATCAAAATGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA/G/ACTGTGCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---			GCACCTCTCCTGTGGCTTGCCTCTGTCCAGCTGCTGTCCAGTGCCACA/G/JTGGTCTAGCCTCATGG CAGAAGCAATTTAGCCAACTCTGTCTGTCTCCACTCTCTCTCTTCCGCGCTGGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ---			GTCACCCCGAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAAACGTGG/G/AJCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTCTG	CAGCTTCTGAC	GTCACCCCGAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTT/CJGTTCTTATGAAGAAGTC AGAAGCTGATAAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCAATTAATAATGAAC/T/CJGGAATAAGAGCATAAACGGACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCCTCCAACACACACACAAATAAGCAGCTAATGGCAATG/AJCTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAATTTGTTTCTCTGATAATGTGGAGAAATCTGCTCTTTATGTA

WI-16879	79 C T	GATACAGGCC ATAATTTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATAATTTCCCA[CT]ATAGGACTCTAGTTCTAGAAAGCCTTGGGGAGAACAGGCCACCCAG
WI-16882	99 A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATGGC	ACATGAATGGCAACCTCTAGGTGGGAGAGACAAATTCCTCCCTTTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTGAC[AG]GCGATTACCTGACATGTGTCATCTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTTT	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACCTTTGGGCGAGG TTC[G]A[TT]AAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C T	ACTGGCCTGT GTTGTTCA	GTCATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTTGGCCTGTG TTGTTCA[CT]CCCACTGCCTAGAAAGATATAGACA
WI-16910	74 G A	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTCTTAAGGAGGTTATATTCGCTATGACTTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA[G]A[GTATCTGTTATAGAAACGATACCTTATTTGGGCCCTGAACCCAGTGAAAGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAACTACCACCATCTCTCTGCTACCACAGAGCAGTAAATCTAGGAATTTGAC TTTACTGCAGCCATTACACCAGCAC[CT]GATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A C	GGAAAGCAGA CCTGGGG	ATGTGATTGOC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAGACTGCAATCAAGGGAAGCAGACCTGGGG[AC]CCA CGGGCAATCACATGAGATG
WI-16947a	58 C G	CATGGAATA GGCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAG[CG]ACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTTACTTTAAATGCACACTACATAACAACCTAAT[CT]TAACTTGGTCCAACTATTT AGTATACTAATATGAGTTTTTATCTGATAACTTGCAATGCCATTAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAGAGCAGTAGAGACTGAGGTAATAGTATT[CT]ACGGCTGG AAATCAACATGCCCTCTTCTCTGTGAAGTTGTGAGCATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60 T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTGCTGCCCTCATCTGAGAT[GT]GTG TAGGACTGTAAAGGAATGTGTTGGGGTTTAGGAA
WI-16992a	46 G A TC	AAGCACCAG AAGTACACTG C	CACATTCCTT ACAGTCTTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTG[GA]CCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTGGGGTTTAGGAA

WI-17010	23 T C	TTCAACAGGA AAAGCCATG	AATAATACGGT GTTTTGAATGT CA	ATGTTTCAACAGGAAAGCCATGTCJATGACATTTCAAAACACCGTATTATTAGAAGCTCATTTAAT TGTTTAAATGCAGACAAATAAAGGCTAACTAAAGCAGATCCAAATGACCCAGTGATCAACCTAGA GGTCCACG
EST17127 9b	74 C T	CACTCGGCAC AGACAGAGT	GGGAGGGCAGG GGTG	ATTCCGTCTCCAAACAGGATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGTCCTGGGAGCCATGGGACCCCTGCCCTCCACAGGCTTCCTAAGTAACAAT
WI-17040	94 T C A	AATCTCTTAT CATCTCAAGCC T A	GGACTATGGCT TATTCAGTGAT G	CACGGCTTCATTAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAAATCTCTTATCATCTCAAGCCAGTCJATCATCACTGAATAAGCCATAGTCCCAGTCTGTTTTCC AAATCTTCTCATATTGT
WI-17044	47 G T	GCAAGGGAT TAACGTATAG G	GGGATCCOCT TGTTAAGA	TTGTTTGTGTTTTTCTCTCTGCCAAGGGATTAAACGTATAGGCTGCTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCAGTCTCTCTGCAGAAATGGCAGGGAATCGAAT CAAAAAGAAAGCAAGTG
WI-17021	62 T A A C T C	TGGACTTGTCA GCCTATAACT A A C T C	TGTAGAGTTAG TGCCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTGACGCTATAACTACTCTTJAGJ CAGCTGCCACTAACTCTACAGGCACAGTAACACTTTATACAGGAGCACATGCCAAAAGTGCCTGG GAGGTGCCAATAAAATCAA
WI-17065	90 T C C T T	CCAGAAAGGA AAAGCATAAA C T T	CCCAAGAGAC AATGAAATCCT GAGATGTTGAA	TGTAAAAAATGTAGACATGGGGGAAAAAACATTCTGTAATCAACATGTGCTGTTTTCTACTTCCGGTA CCAGAAAGGAAAGCATAAACTTTCJAGGATTTTCTGCTCTGGGT
WI-17066	32 A C T	TGTACAGCCA ACATCACTGT A	AATGTTCTGGA A	TTCTAAGGTTGTACAGCCAACATCACTGTTTJACJATCCAGAACATTTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCACTCCCTGTAGTCTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86 T G ---	---	---	TGCTGACTGTCACTGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAGGAT AACCTCTACACAGGCCCTTJGCTACATAGGAGTATATTTGGCCAAAGACTACCAGTAGAAGTGATT
WI-17104b	108 T C ---	---	---	CAGATGAGAACTCATCTGGCTCATCTGCAAGCTTCTTGATGCTTTGCGAGCTTCCCATTCATTCCA AATCAGAAAGCAGTCAGTGCCCGCTGTTTCCAGACGGCTTCTCTCTTTGTTAAGAAATTA
WI-17114a	37 T C	TTTCCATCAAG GACTTGTGTTT A	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGATGTTTCCATCAAGGACTTGTGTTTTJGCTCTCTCACTGCTGCTATTATAATAC AAGCTAGCTCCCAAGGCCAGATGCTTAAGTGTCTAAAGAAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76 T G C T C T T	GATGAAATTC AGATAGTCTTC C T C T T	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCTCTTTJGJCATACTCTCCAGGATCTCGAAGAGGCCCTCTTTGCTGCTCTAATTT
WI-17163	43 A G T A C G T T	CATTCTTTGT AAAAAACA T A C G T T	CAGAAATCTTGC TTTTGCCCTT	GAAATCGAATACGTCCATTTCTTTGTAAAAATAACAATAAGTTTJGJAAGGCAAAAGCAAGATTCTG TAAACCAACATTGGAAGGGGACACAGGGAGGGGCAAGGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA

WI-17178	127 T C	GGACTCCCTCA	CCCTCAATTTT	AGCAATGTCCTCCCTCAATTTCAATAGCTATGATGGAGTTATCAGTTTCATTTCCAGAGCGAATTACTGGG
WI-17180b	81 C G	CTGAGGAGC	CAACTGCTTC	GGCGAGGGGGTTTAATATCCTGATGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA
WI-17180a	47 T C	GCACAAAATA	---	GCAGTTGAAAATTGAGGG
WI-17156	54 G C	TAGAGAAATCC	TGCGACGAGAC	TCATGGACATCCTGAAGCAGACACACAAAATATAGAGAAATCCTGCACCTCCCAAGTCTCGTGGACAG
WI-17149b	79 T C	CTTTAGATATC	TTGGG	GCCTTCAACAATTACCAACATCTTGCCCAATTTGTTTCAATTATCCGCAACCCACACTGACAGATGAG
WI-17149a	48 C G	CAAGGTTGA	CAAGAAATAT	GGAGTC
WI-17197	67 G A	CTGGGGCTAC	GCATACC	TCATGGACATCCTGAAGCAGACACAAAATATAGAGAAATCTCTAACTTTAGATATCTCCCATGCTCCACAGA
WI-17198	38 A C	CTAGTIT	ACTGAGAAATT	ATCAAAATATATTTCTTGGTTGGAAATTTTAAATGTTCTTAACATCTGCCTACCATCCACCTCAAT
EST18753	27 C T	GGTCTCAT	GCCTGA	TAATATCTTG
WI-17108b	74 C T	CAAAAGTAAA	CC	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATGCTCATGCACGTGCGTGGAA
EST19067	41 A G	---	---	ACCCAAATTGTGATGTATGAACATACAAAGGATGGGAAAGAACACATTTCTCTCACA
EST19067	2b	CGTGACCAATTT	AAAAGTTGAA	ATTTGCTATGTTGCTGGGCTGGACTCCAGCAATCCTCTGCCTCAGCAGAAAGTAGCTGGGGCTACIG
EST19125	40 A C	TTC	CCA	/AIGGTATGCACCACTCACCCTGCTTATCAGTTTCGTTTAAAGAAATATTTAGATTTTAGATGGCA
8	28 A G	---	---	TGATTTTCAGTACTTTTCTCCCTGTCCTTAGTTTAC/JAATTTCTCAGTGGACAAATGGACAA
				ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC
				TTC
				TCGCTATGCTACCCAGGCTGGTCTCATGCTCAGGCTCATCGATCCTCTGCCTCTGCAGTGGCTGG
				GATAAGACACAACCTGCCACCAGGCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
				TTATTTTAAACATAACCCAGATGCACCTTGGTTTTTACATTTCTGTTGCCATTTCAGTCTCAAAGT
				AAACACGCTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACTTACAGAGT
				ACACAAAATTTACCATGTCGACCAATTTAAGGGTATAGTTCA/GJGTGGCATTAAAGTACATTTCAACT
				TTTTGAGCAACCCGCCATCACCATTCAATCATCCATCTCCGTT
				ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JAGTGGCATTAAAGTACATTTCAACT
				TTTTGAGCAACCCGCCATCACCATTCAATCATCCATCTCCGTT
				CTGTTTCTCAGAGATGACACTGCCAACA/JGJTCACAGATTTTGCATACAATACAGTTATGTATTGGC
				TATTCACAAATTTACAGTAGTGTGTTTTTCTCTGAAAAA

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EST20824 8	115 T	AGTCGGAGT GCTGATTG	AAGATTTTATC TTGGACCGA	GTGTGAAGCCGGAGTTTATTATTATTCAAATCAGTCTCTCTGAAAACCTCAGGGATTGAGGTTTATA AGGATAACTTGGTAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTG[T/G]JCGGGTCCAAAGATAAA ATCTTAGG
WI-17347	50 A	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCT[G/G]GTAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGAGTGGGACCA
EST21904 b	128 G A	TTCATATGGCC ATTTTAATAA G G G	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGGTCTGGGAGCAGGTGGGCAGTTTTCAGTGAGGAGCAGGAAAGTAGACGAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTATATAGCCATTTTAAATAAGTG[G/G]ATA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTCTT	TGGAAAAACA GCCCCAC	CAAAACAATGTAGACATAAGGGAACAAATTCAGAGAGGTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATTCTT[T/G]GTGGGGCTGTTTTTCCAAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCTCGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCACCAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATATTCTGCT ATTCCTGCCATT[C]ACCCGATCCTTCATGGTAGAGTATCACAAAGTAAAAGTTTCTGGTTGTTTCATC TACTTAAAACCA
EST22311 9c	92 T C	---	---	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCCTGTAAACAG TAGCATTCATGTTTACTCTAT[C]GTCAAAAGCTGGGCAAGTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G	---	---	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCC[C]G[C]CACTGTAAA CAGTAGCATTCATGTTTACTCTATTGTCAAAGCTGGGCAAGTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATAT[C]ACATAAAAAATCCACCCTGTAAA CAGTAGCATTCATGTTTACTCTATTGTCAAAGCTGGGCAAGTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C	---	---	TGAGGAGCTCTGAGGAG[C]CACCAGGGAGCTGTGTCCAGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTTCTCCTTTTACAAAACCTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTTTAAGTGT
EST22433 c	103 A G A A	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA AGTTTCAGTTT	GATGTTAATGACTTTCTTTGAGATATGATGGAAAAATATTCAGGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC[C]G[CTGTG]CAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA	GCATGAATTT T	TATCCATTTCAAGAAAAAAATGACTTAAAAATACAAATCTATCCAGAAATGGATCCTTATCTG CACAA[G]GCCATTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTT

EST22993 5b	71 T C	ATCCTTTTGT TCTACCCOC	TTGCCTGTAA TTTGACTGTAA TG	GCCTTTTATGTCTCTTTTAAACATCAATGTTTTATAACACACTTGATCTTTTGTCTACCCCA ATT/CJATTACAGTCAAAATTAAACAGGCAATATAATAGGCTAACAGAAATGCTTGCAATT TTATTTCTCAGCTTACCATTGTGTACTTATATCTGTACAAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTATTAATCTTTGCCTTT/AJATGGTTTTGACAGTTTGTGCTTTCT T
EST23021 0	108 T A	---	---	ACAGAAATTTAACATGCAAGTTTTCATTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTCTTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAGCTCCAGAGGCAG/CJGCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTCACTG
WI-17387	55 C G	OCTTTGCAGAT TGAAGAAAAA	GCITTTGCCTA AGATTAATAGT AACTACT	AAAGGCTGTAGTTTGTGTTTTTGTCTTTTCTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	OCTTCCCTCC TGTAAGC	CTGACACGTCCTGTGTGCGGGGTGCTCATGTGCGGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCT/GJTCGGCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGAAA TACCATCAGCCTCC
EST23733 9	31 T G	GGCTGTAGTT TTGTTTTGTTT CCAG	TGCACITTTAA TCCCATCAAT	TTTTAACGAAATCTCACTACTGCAATGCAATGCTTTGTCTAGCTAATGAATGCA/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGCTTAGAACAGTACATGGTGCAATAG TCTTTGATACAGGTAACCAAGTTTTGTAACTATTATCAGAACTTCACTGTATCTTCAAGTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/CJGTATAATGTCAACATCAGGATTTCTTTTT TCTTTGATACAGGTAACCAAGTTTTGT/CJACATTTATCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGTCTATAATGTCAACATCAGGATTTCTTTTT GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
WI-17519	55 T C A	TAATGAATGC	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
EST25356 3b	95 C G	---	---	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
EST25356 3a	26 A C	---	---	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT CATTGATAA	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCTTTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	---	---	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC

WI-17623	46 TC ---	---	TGTGTTTTAAATTTCCCATATAATTAATGGTGGGCACATTT/CJGCATGTGCTTACTGGGTC ATTCATATATCTTTTGTGAAGCATCTGCTCCAACTCTTTTGCTGACTTTGGAGTTTTTGGT
EST26419 1b	46 TC ---	---	ATTTACACAGAGATACAAAGGCAACTAIGTCAGCAACAATCTGAT/CJGGGCAGTCCAAAACCTCT TGGGAGGAAGTAAATTCATGTGTAATGTCATGATGGCTGTTCCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	35 C/A AG	CAAGAAGTTTG GACTGOC	ATTTACACAGAGATACAAAGGCAACTATGTGCAG/C/AJACAATCTGATGGGCAGTCCAAAACCTCT TGGGAGGAAGTAAATTCATGTGTAATGTCATGATGGCTGTTCCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780 5	69 GC ---	---	TCAGCTTTAATTTAAGGGACATGTAATAAAGATGCATTTGACAGGACGACGACTAGTTCAGAGC AG/CJAGGTTAGACCAGTACAACAACCAAGAAAGCAAGTGCCTGTTCCATCTTGGCTTTACCA CACTTACAACTGATACCC
EST26900 7	39 A/G ---	---	TACTTCAGTTTAAGGCAAAATTCACACAGAGACTGTCTC/AJGAGACGGGCACAGAACCAGACACC GTAGAAACACCACCACCATGTCATGACGGGAAGCAGAG
EST27152 1	101 CT ---	---	CAAAGGATTTATTTTGTCCCTAAAAGTAAATCTAGAAAATAGGAACCCACTGCAAGAAGAGTT CTATACTAAACATTTCAATCATCTCTCTCT/CJTTCACATGGTGACTCTTTTCATGTACACAT CATCGGAAAACAGACTGA
EST27504 0a	33 G/A ATTT	GCACTTTGCAA CAATTTAATA G	TTTTGACATTTGCAACAATTTAATAATTTATC/AJCATACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTtaggcaaaagtctttcagiatcttctgttacacattctgttaacaagaaccccatatactt GGTAAATTCATCT
EST27662 4	51 CT CTCCAGTCTTG C	TTATGGAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTCTGTCTCCAGTCTTG/CJAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTTCTTAGAGTAACACACACTCTTGTTTAGGAATGTTCC
EST27788 3	100 A/G ---	---	ATTTATTAGCGGTACAAATCCAAAGGTGTAAGGGTGAAGGAAAGGCGAAGGCAGGCAAAATACAT TATTGAGCTGAAAACAACATTTACATTCAAGGAC/AJGCTTCCAGACAAGCCCATGTAGAACCCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G/A AGA CCCCAC	GTGACAGAGAGG TACTCCAAGTA C	TCCTTAAACCTTTCTCTCTGTTGGATCCCAAGTACAGTGGAGTCAACAGAACCCACG/AJGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAAATTTACTTGAA
WI-18369	58 G/A ACAATC	AATAAATTC AATCTGTAC G/A ACAATC	TAAAAATTTGAGATACATTTCCCCAATGTAACAATAAATTTCAATCTGTACACAATC/G/AJAAATG GATAAGGCCTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTATCTC TCCCGCTTCCAAAAGCTTTATTGGCAAATATGCTCTA/CJAAAAGAATGATCAATCCTGTTGCCCTC AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACCACGCCGTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTATTTCATAG
EST28036 4	37 TC ---	---	

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT	TTCTCGCATT TATTTTATAC CA	CATTGGAGTAAAGGTGTTCTTCTTTAAAT/AJATGGTATAAAATAAATGCGAGAAACATTAAAC GGAGATGTACAGACACAGACGAAGACATGAGTTGTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50 T C	TGGGCTCC TGTC	TGGGTTGGCAG TGTC	AGAAITGGTCTAGTAATCGTTCAGGATTTGCGTGATGGCCCTCCCTGTCT/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACCTAAGGCACGTCATTTGTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACACAGAAAGTGAAGTCTATT/CJGTTACATCATACCAAGTGATACATA TT/CJACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT	TCAACAGCCAT AATCATGTG	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTCTATT/CJGTTACATCATACCAAGTGATACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACATTAAGCATCATTGTCACT[G/A]GCTAACTCCT CAAATCAACAATACCCCTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTAGAAGGACACCAGCTTTGTGGACTTAGGGCCTACCTATTCCAGCAGGTGCC[A/G]TTATTT TCACTTGGTTACGTCGTGAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTG TCATTCTCTG T	ATTATTAGGTATCTGCTGTTGGGGTGGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT[C/T]ACAGAAAGATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATAATTAAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCCCTG
EST30223 2	99 A G	---	---	AAATAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTTAATAATTCC[A/G]GGATTAAATTTCTTCTAGTTCATCTTGGGA GG
WI-16260b	86 G A	---	---	CTTTCCATTGGTATTAACTGCTAGAGGTTCTTTGTGAGGTGGAATCAAGAAGAAAGACCCAGA GTTTCAATAATAGGTAGC[G/A]ATAACCAAGGCTCACTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA	CTACCTATATT GTGAACTCTG GGT	CTTTTCCATTGGTATTAACTGCTAGAGGTTCTTTGTGAGGTGGAATCAAGAAGAAAGAA[G/T]ACCC AGAGTTTCAATAATAGGTAGCGATAACCAGGCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT	TGGGTATAGG AACAGGC	AAGAGAAACAGGAAATATTGTCTTCTTGTG[A/G]GCCTGTTTCTATACCCCAATATCATAAGAAAT GTTGTTGCTTCTATATGTTGAGCTTCAAAATCTTTTGTCTTAATCAATCCAAATGAATTACCTGAAT TTCTCCTTGTGTTCAAAA

EST31951 4	87	C T	GGGTTGTCAG CCAACA	CCACCAAAAT CACTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTTGCCAGCCCAACA/C/TGGAGGTGATTTTGGTGGGAATCTTATCACAATTATCT
EST31968 8b	95	T G ---		---	CGAATTTGTCTCTCTTATTTTGTGATTCTAGTAATCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT/GJAACCTGCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75	T C T .	GCGGTTACTA TAAGTGCATTT	TGTAAGAATCA GTGGCAGTT	CGAATTTGTCTCTCTTATTTTGTGATTCTAGTAATCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAACCTGCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCCC
EST32063 2	103	C T ---		---	TCATGGATGAACAGACGCTACATGCCACATCCCACTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TGTTTCAGGCCCATTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G ---		---	AAGGCTTCCAAAGCATTCAAAGGCACCTTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCC/AG JTCTGATTAGGGAGCACCCCAAGCCCAAGTAAATATGGTCTTGCAG
WI-17800	29	C G GAGAACTCA	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACTC/GJAAGACTGGGATTAATTGTAGGAATATTTTCACAG TTTCCACAAGTCAGAAGAGAGTAATCCCAACCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTTC	TGGCTTAGGT TCTACTTGATG T	AAACTGTCACTTCTAAAGTCTGGGATGACTTTCCT/GJATTCTACATCAAGTAGAACCTAAGCCAAAT TCAGAATCAGAATCCTTTTGTCCATCAAAATCCAGTAACCTCAAGCTGAATTAATGTTTCACTCT
WI-17860	121	T A AGCAAATA	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCTGTCATGATTATTTGCTATAAGGAAGGGGAACAAAATCTTTA TAGTGTCCAAAGATAATTAATCTTGTTTAAATCTTTGCCAGCAAGCAAAATAT/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A T ATTGTT	TTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTTTTTATAGCCTACTTCTCAAAATTTGTT/A/TJTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAAACTACCA
EST33301 4c	80	G A ---		---	GAAAAAAAAGTCAATGTGTTCCCTTTATGGGTGATGCCACCATGATTCCTCACACAAGCATGATC AATCGCCACGAGA/GJA/ACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A ---		---	GAAAAAAAAGTCAATGTGTTCCCTTTATGGGTGATGCCACCATGATTCCTCACACAAGCAT/GJA/
EST33460 1	44	G A CA	AGCGTGGTTTT CAATACTAAA	CTGTATTTATT GTTAAATATTT GCATTGTT	ATCAATCGCCACGAGAGACTGATGCCAAAGAGTATGG CTATCCAAAGATATTTATTCAGCGGTGGTTTTCAATACTAAACA/GJA/JGTAAACAATGCAANTATT TAACAATAAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAACTACTTTGCAA

WI-17904	50 A G A C A C	AAAGCATGAC AATAAAATGA	CGCTTATGTTA ATAGTAATTCG CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACATAAAATGAACACAG/GJTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACAAACAAATGA GTTTTTCTTTGAGTGACACAAGCTGTTCAITTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TIA/GIGATTTTATTAGTTGTTCTCGCTAGTAGTTTTGGTATTCTATGAAAAAAGCAGCTAGTTCCAGC TTACAAATCACACAAGT
EST34149 5	69 A G A T	TGCCAAATAC TCAAGTGTGA	AACACTAGGG AGAACAACTA ATAAAATC	TGGGAAACATAAGTTAACTCAAGAATATATCCAGTCTTTATGTTACTAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC/AJTACAAAGATTAAAGAACTTACCATCAAAACACATTC CAGTGCATCAA
EST34343 8	95 C A ---	GGACCATATG ATATATAACT	--- CAGAAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTTAAATGGAAGGAACACAGGTATGTTGAAAGAACATCAGTACAGTGGAGACAGG GAGGGACCATATGATATATAACTCTCTAAAGC/CJTJGGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTCATCA
WI-17982	98 C T C C T A A A G C			CTCAGTAACCTCCGGTGATATAATCTGCCATTTATTGATTTATGATAAAACACCTCTCATTTGTGA AAACACAGCTAAGGGTGACATCTCCAGACCCAAACCAGTGTCCCTGTAATGTACJCTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17993	118 A C ---		---	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAAACACATCTCCCAGGCCCTCGCAGT AGAGCGAAGGGAACAGAG/GJGCTGCCATGTGCCTGTCTCTAAAGACGCCACCTCAGGTTGATGT CACCTGTGGAGACCGGGT
WI-17996	84 A G A G G G A A C A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	ATTCCTTTATAAAACACCATGTCCCTAAAATGT/CJATTCACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-17136	33 C G ---		---	GCCACTGAAAAAAGGTGCTCTCCACJGCTTTCTAACTCCCTGACTCCCTCATTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATAGCTTAATCA
WI-18041	24 A C ---		---	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCCJAGJCTTGA GATTCAGAATCCAGAGGGTCTCAGTCCCTTGGTTAGGTCTTCTGTGACATTTCCCTCTTG
EST35164 8a	57 A G O O C C	CACAGCCCTGC O O C C	CCCTCTGGATT CTGAATCTCAA	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTGGTTACACATCTTAG A/GJACAGCAGAGCTGCCCTGAGGGAGGGTTGTGTTTAAATGTCTGATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052b	67 A G ---		---	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTGGTTACACATCTT AGAACAGCAGAGCTGCCCTGAGGGAGGGTTGTGTTTAAATGTCTGATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C A T C	CCTGAGTTCCT TCATGTACGA	CTCAGGCAGCT CTGCTGT	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAGJATGGAAGCAGGGGTGACG CATGCAAGGAGTCCAGACAAAAGACGGGTGATTTTGTCTAGGTTGGTAGCAACAGAGGTAATG
WI-18054	46 G A G A G T A A A A	GGGAGTGGG GAGTAAAA	CGTCAOCTGC TTCCA	

WI-18064	54 G A	GTAGTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCTGTGGGTAGCTGTCTAAGCTGTATTTCAGA[G/A]GAATGTAC AATCATACCACTGGGAGAAAGAGTAAGCACAGTCTTATTAGGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCAAC TGCT	TTAGCACCACTTCTAGTGGAGCAGGATTCTTGATCATGGGTGGAATTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT[C/J]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C G T G T A T	AACCCACTAC TTACTCAGAGT	AAAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT[C/J]ATATTACACATGAAAGATAATACTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAGCAATTTAGGTTGCAAGGATATAA
WI-18080c	80 C T ---		---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTTTGTAAATTAATCTACTATGCCGTG TTTGACTTTTAT[C/J]TCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080b	65 G A ---		---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTTTGTAAATTAATCTACTATGCC[G/ A]TGTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080a	41 T C A G T C T C	GCAATATCA ATATCAAAC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCT[C/J]TTGTAAATTAATCTACTATGC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18086	63 G A ---		---	GTGGGCATCTATAAAGCAGCCATGTGTTGAACAAATGATATGCACAGAAAGCATCTT[G/A] TGGCTTTGTTACACGGTTTCTTCAAGAGGAAGATGACTAGCCCTCCAGCTTCTGCAGCTAGC TTAGGAGAGGTGTTGAA
WI-18115b	71 C T ---		---	AACTACATAGTATGGTGCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTACCTTTGGTATCCC TTC[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18115a	70 C T T T	TTAGTGACCT TTGGTATCCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTACCTTTGGTATCCC TTC[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18136	78 A G ---		---	TTTTGAGAAGCACTCTGTAAAGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTTTTA GGTAATTTGG[C/J]TAAGAACATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT
WI-18169	115 A G G A G C T C	CCATCTTCCG	GAGTTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGATCTGCCCAAGTCTTTCCACTATGAAGGCAATGTAGAG TGTCAGGAGGAAAGGTGTATCCAGCAGCCATCTTTCGGGAAGCT[C/J]GTGGAGCACAAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18190b	26 G A ---		---	TGAAAGAGTCGACACAGCGGACACT[G/A]TCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAATCTCGGCGA

WI-18190	62	G A	---	---	TGAAAGAGTCGACACAGCGGACACTGTCTATAAGTGGAAACAAGGATGAAGCTAATCATGGA[GIA] GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGAATGAGCTGGAGACATTAACTCTGGCGA
WI-18181	100	A C	CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAACAACATTGAAACACAAATACAACAACATTAGGAACAAGAAATGTGTAATCCAA TGTGTGAAAAATATATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAAACGTA TGTGTTCTTGAAC ATTACATAAAGCATTTCTGAGTACAACACTAGGGGACAGGTATTTTCAAAAAACAATAGAGCAGA GTTCTGCCCTC[G/A]GTGTGCGGGGAGAGAGGGGATTTCAGCATTTTGGTGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18215	78	G A	CTGCCCTC	AGCAGAGTTC CTGCCCTCCT CCCC	CATTCCGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/GAA CCCTGAAACCTTTATTTTGAATTGAAGTTTTGCTCAGAACTGGGAGAACTTTTCACATTCTG AC
WI-18232	60	T A	AA	C	TTTAAAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATAT[C/T]GTCTCACTAGTCTATTCACCTCTGTGGCATTTTCGGCAGAGTGGC
WI-17892	76	T C	ACA	GAGACA GCTAACACTTC TACTGTAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAAT TGGATGCCACAACCTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAAG GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266c	119	C T	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T C	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C T	TTCAAA	TTTGTGCA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A G	AA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTGGATATGTGGTTAGTGTCTATCATTAATTTGGAAAGCTGCAGCTATTGTTATTC AAAT[AGTATCTTCTGCTCCCTTTCTCTCTTTCTGGGATTCTCATTTCTGCATGTGTTATA AAACATCTACAGCTGCTTAGGCCATCTCTGTAAGAAATCAGGGATAAGAGCTGAGGAAACAAGAGG A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAATAAGAACATAATTTTTTTGTTGAT TCACA
WI-18330b	66	A G	---	---	

WI-18330a	49	G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTAGAAATCAGGGATAAGA/G/AJCTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAGAACATAATTTTTTTGTTGAT TCACA
EST37564 5	85	T C A G A	AAATTC AAGC CATCTACAAA	CTATGGAGGOC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATT/CJCTCATTTAGGCCCTCCATAGGCTGCAAAACACATCAAAAGGCATTAC TGTA CTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTCCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTTCGTTAGGCTAGT/G/AJGCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	G A ---		---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGACGCTGATGG CCTGCAGTCCTCTGCCGTGCTTGGCTCTCTGGACG/G/AJTCATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
EST37624 6a	58	C T ---		---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCA/C/TJGCTGA TGGCTGCAGTCCTCTGCCGTGCTTGGCTCTCTGGACGGTTCATCTACATGSGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
WI-18357	89	C G G C A T C A A	CCCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTCTACCGTGTGAGGTGCCATGAAGCCAAAGCCCATGGAGAGACATTTTCAGA TAATCCCAGCCCTTAGCATCAA/C/GJTCATCTTCAGTCTTTGAGTCTTCCAGCCAGGTCCAAAGCTT GTGGACCCAGAGACAAGCC
WI-18012g	117	A G ---		---	TTTTATCTGGGTGAGCTCCTTCTTAATGGCCTGAAGGTGATCTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTC/G/AJTGAAAGTGTTCCTGTATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---		---	TTTTATCTGGGTGAGCTCCTTCTTAATGGCCTGAAGGTGATCTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTC/G/AJTGAAAGTGTTCCTGTATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T T	GCCACTTTTGC C C C T T	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTGAGCTCCTTCTTAATGGCCTGAAGGTGATCTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTC/G/AJTGAAAGTGTTCCTGTATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---		---	TTTTATCTGGGTGAGCTCCTTCTTAATGGCCTGAAGGTGATCTCCTTCCTTTCCTCAACTTTCCAGACTTGGAA AGATCCCCGTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCCTGGAAGTGTTCCTGTATACA GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA CTGATTAATAA	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCAATTGT/G/AJATTAAGTTTATTAAATCAGCTGACTTTAGCAATTGGGAGATTATCTGGAT

EST38512 7	91 T G	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAAACTGACCCAAATTGGTAAACTGTGCTGGACTGAGAGAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTTCGT/GJGCTTCCCAGAGTGCAAGTGAATACTGTTATAGCC CCTGCACCTCCTAAAGATCTTTTC/TTJCCCCCAAGTCTAACAGAATGGTATATCTCTCGAAAA AGATGAACGTCATCAATGGATTGTGCTGCTCTGCTTTCAGCTTTGATTTTTTTTGCTCTTGAGAACCTTG TCCTCCCTGCTGATT
EST38519 0	24 C T T	GAACATCCCA TGTTCTGTTT	TCTGTTAGGAC TTGGGGA	AGTGGTCAATGTAAACTAATGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTTCTGTTTAAI T/CJTCTCTTATGTGTATACCTTCCCTTCTCTTTCTTATACACATAGATTTTCTTAAATGCGAGC CCA OCATCTAGGCAGGCTACCTGAGCTCTGTGCTCCAGAGTGGTGCCTCACGCCCGGGGCCCGGTGG AGTCTCGCGGGCCCCCGCTGCTCGCCCTTC/GJGCCACCATCCATTCTCCAGGGG
EST38575 1	66 T C A A	CCTGCTCCGCG CTTC	GAGGAATGGAT GGTGGC	TATAGTAGGTACTTCTTCTGCTGCAGCAGGAATTAATTCAGTCTGAAGTGGGCATTTCAA/T/CJGCGTG GTATTTTTTCTTTTCATTTTTTGCAAGTAAAAAATCAT
EST38616 9	101 C G C T C	AATGGTCAITTT TAATATATCA GTTTTACA	TTGCAAAAATG AAGGAAAAA	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATAT/CJAGATAGAAGATTAAGGACCAT CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTTGGACCCAGGCGGTTGGTTCCAGCATATA GGATCCTCACTCACTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTCCCCJAG/JAGGCCAGCGGGATGTGTGCCCTCTCTCCCAACTCATCTTTCAGGAACACGAGG ATTCTTGCTTTCTGGAAA
EST38652 8	59 T C C A T T T C A A	TGTCOCTGGA GGTGATATGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTTCACTAGAGGGGAGAAGTAATCACCTACCTTTTGGATGCCCTCCACTCTACTTGT CTCCCTGAGGTGATGG/JAGJCTTAAAGTCCACGATGGTGACCTAACTCAGTTTAAATCTTGGC TAGCAGCAAC
EST38654 5	42 T C G T T T T A C A	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGQT/JATTTGAATTCAGAGCAAAGCCCT CTTACTGAGAGGTGAGCCCAAGCCCTCCAAATGCCCTTTTCAATGAGTAGGATCTCTAAGTGTGAC AAACAAACCAACATGGTGG
EST38707 9	75 A G ---	TGTTATGAGA ACCCATTACA CAICA	GCTGACTGGCA CATGCTTT	CACCCCATATTGACCAAGGATGAAGCCTAGCCATGCTCTTTCACCTATGTGTGTTTCAACAAG TGTTTATGAGAACCATTACACAC/JAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38759 2	86 A G G T G A T A T G G	CACGAGTAAA AAGAAACTCA TGAC	GGAGCGAGTGC AAGGAGAA	TCCTTACTGTGCTTACAACCTTCTCCCAAGTTTGGGGTTCATATTTGTTATTTGTTATTA TTCAACACGAGTAAAAGAAACTCATGAC/JTJTTCTCCTTGGACTCGCTCTCCCAATCTCGAT ACCGACTGCACTGTTG
EST38775 1	40 T A C	GCTGTAGAATT GCTGTGATGC	GGAAGGAOAG AGGACACAG	CCTTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTG ATGCT/CJGCTGTGTGCTCTCCGCTCTTCCCCAAATGAGCACATATGAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA
EST38815 4	91 C A C A			
EST38858 4	98 C T T G A C			
EST38865 2	72 T C T G T G T G A T G C			

EST38878 9	47 T	AAACATCATT ACTAGCCTAG CATCCTAA	CCTCAATAAA TCTCATGTCT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAAT/CJTGAGGACATGAGATTT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGAAATTTGAAACATTTCCC TTATTCAATGTCTCATCTACACATTCITTTATTTTATTTTCTCACTTTCTCAAAATATCGGATTGTGC TCATGAGAAATAATGGCTGAGGAGCTGGCAGCGAGTCTTCTCA/GC/GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATTCAATGTCTCATCTACACATTCITTTATTTTAT/CJTGTGTTTCTCACTTTCTCAAAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTCITTTAT TTTT	CGATATTGAG AAAGTGAAAA CAA	TTATTCAATGTCTCATCTACACATTCITTTATTTTAT/CJTGTGTTTCTCACTTTCTCAAAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38909 5	47 A G	GCACAGCATG GCTAAACG	GGTATTGTG ATCCCATCTT T	GCACTAACTAACTTTTCATTTGTGGATTGCACAGCATGGCTAAAACG/A/GJTAAGATGGGAAATCAAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A G C A C	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	AACTGAATGGCAGTGAACAACTACACATCAAACTTAGGGAATGTGGTTAGTGTGTACGTTGAG GGAAACTTATAACCTCAC/A/GJGCTTGTTCACAAAACACAGCAGACACAGAGATTTCCCACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C G G T G G	TGAATTCCTT GGTGG	CACGTGCAATCT CAOCC	TAAACATTCCTTGAATTCCTTGTGGG/GC/GJGGGGGGGTGAGATTGCAGTGTCAAGATAAA TATCACAATATATCAAACTTCAAAATGTGTATGCAATTCACACACTGACATGAGCCACAAACAT CCTTTCACAGGACTGTAC
EST39002 0	42 G A T G A C C	GGACCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGAGATCCCGGACCTTCGGTGAACG/A/CAGGCTCCCTGCCAGGGCTGG CCCTGACCGGGCTCCCGAGCTCGGCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G C C T A A G G A A T	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG GGC	CACGTGGCCCTAAGTTTCCGGGTCTTCTCAGTCTGGATGGCTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAAT/GJAGGGGCGAGGGCGATGCCGCCAGCGAGATGGTCTGTAAAGCCTGTGGGTG AAGACCTAACTTCTGGA
WI-16398	90 T C T C A	TCCCTATTATT CCATGATATTT	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAATGTATCATCAACGCAACATATAGAAACATAAAAGAAAAATAAAGTATCCACCCTAAAAAT CCCTATTATTCATGATATTTTCA/T/CJAGCAACTAGTATATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C A C T	CCTTGTCTC AATTTTAAAC ACT	TAAGGGTAAT TCCCTATATAA AAAG	GGTTGTCTTTCATGTATTTTCTCATTTCTCATCAGTTTCTGGTCTTTGTCTCAATTTTAAACAT T/CJCTTTTATATAGGGAATAGCCCTTAACTGTGTGATACATGCTGCCAAAATTTCTCTCCAGTT
WI-16406	24 C T A G G	GCITTAATGGC TACAGAAAGA	CCAGAACCAG ATGTGTTTAA AA	GCITTAATGGCTACAGAAAGAGG/C/JGGTTTATTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCAATTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G G C T	TCATCTGAGA ATAAACTTCCT	CATTATAGGTA CTGAGTCATAC	TTCTTTTATTCATGATTGTTTCATCTGAGAAATAAACCTCCTGCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAATAATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T G G A T G C C	CCTGAAACAG	GCACAATTAA ACATAGTACCG	CAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTGCTGAGCCAGCAACCTCGAGTTACCCGGCCTTTACCCACAGCC AGCTCTGCTTGCTGTCAT
EST39366 2	72 T C ---		---	AGAAACATCTCTGCTGATCAGAGGAAGATGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTATT[C]ACACTGAGAGGAAAATGGAAGAAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGTTCAGA
EST39371 9	86 A G G G T G A G A G G T T	CATTGGATTAA GOGTGAGAGG	TGATTTGAGAC ATTCACATTT	AAAAAGCTGTAGCTGGCAAGTCAAAAGTTTATTTATGTGTGTAATTTCCAGTTGAGCAATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAATGTCTCAAATCAAATGCTTCTTCTAAAGATTA GACATTGCCCAACCCCTGC
WI-17177	23 A G ---		---	ACAAGTGACATATCCAACCAAC[C]A/GTCCATCCCACTGTGCCCTATTCCTTCTGTGTTCTTT AGAGCCTTTTTCAGCTATTTCTGTGTAAGCAAACTGCACGAAGGCCCTCCCGTACTCCTCCCTGGAA G
EST39428 8	31 C T A T T T G A T T	GCTCCCCACA TAACTGATGTT	GGTCCCTTATG AAGCCACC	AGGTTCTGTGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCGCTATT TTCTGGTGGGCTAGGTAATCTGTGCTTGGTCCACAGAGACAAATTAAGAAGATCAGGTCT GGCTGTTC
EST39430 2	45 A C C	GGCAGAGGAA TAACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T G A G T A A	CTACTGACAT AGGACTTCA	TCCTGGAAAAG TGACATAAACCC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAAATAACAGGAACCTATTTATAT ACGTAATACACTTTTCATACCTGCCTACTGACATAGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTCCAGGATTGTTCTCCC
EST39465 2	80 A G G T G C C	AATGCAGGAG GGTGGC	CAATCTGGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGTGG[C/A]GAGAGGGCCGAGATTGGGTGTTCCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G A A C A T T A G	AAAGATTCCCT GTAGACATCT	CACITGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTGACAGACTTTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C ---		---	CACAAAATGGGACTGCTGAAGAGTGACAGTTGGACCTTACTTTTGGTGACCCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGTGTAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGATG GCTATGTAGACATAAGA

WI-18387a	57	A G	CCTTACTTTGG TGACCCCAT	GCTAAGCATG TGACCACAA	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACIAGITTTGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAGTGTATGTGCGGATG GCTATGTAGACATAAAGA
EST40601 9	78	A G	GCGTGGAAACCT GAAACAC	TTCTTGAAGA AAGGCGTC	TCCAGGATGTTTATCCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGGTGACTCGCGGTGGA ACCTGAAACACIAGIAGCGCTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
			AGTGATCAC ATCTTCAGGAT	GCACACCGTTC ACACTGTTA	TCATTCAGTGTATCACATCTTCAGGATAGGTIAGIATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTGA
EST41935	32	A G	AGGT	CACTGTTA	
			CATTCTGGTCT TTATTTTGGGA	AAACTGATTT GTTAAACATG	ATGTCATTCTGGTCTTTATTTTGGACACIAGTGTAGCATGTTTAAACAAATCAGTTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATATTTTACAAATTTCTCATCTACTGTAAATTTCA
EST43091	28	C T	CA	CTAC	
WI-18420c	108	T C	TTCCATTAAAC AGGAAGTTTC	AAATTCACG ATTGCTATAAG	AGAGAGACAAACAAAGAATAAGGGGAAATGGGAAGAACACAGAGTGAATTAAGCAAATCTTTGGA TTCCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAAATCAAAATCIGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
			GAATAAGGGA AAATGGGAAG	CCAAGATTTC TTTAATTTAC	AGAGAGACAAACAAAGAATAAGGGGAAATGGGAAGAACIAGAGTGAATTAAGCAAATCTTT GGATTACAGATTCCATTAAACAGGAAGTTTCTCAAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38	C T	AA	TC	
WI-18425b	101	T C	---	---	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGGAGCCAAAGATCAGACACCTGTG CTAGACAGATTCAATGCACACAAACACAGGAGGTCACCGGGGTCACCGGGCGGAGAGCCAAAGAC TAGGGC
			CACCTGTCT AGACAGATTTC	CCTCTGTTGT TGTTGTGA	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGGAGCCAAAGATCAGACACCTGTG CTAGACAGATTCAATGCACACAAACACAGGAGTGGGGTTCACCGGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81	A C	A		AAATTGAGGTCGGGTGGAACTATAAAAGGAAAGGAAAGAGAGTAATCAAGGGAGGCCAAAGTG GGAAGCTGATTGCTGATCTAACGTGCTGTCTCCAGTTCTTTTGGCTCTAAGTGGGACTACITTC TGGATACAGTCAGGGGAG
WI-18449	129	C T	AAGTGGGACT	CTCCCTGACT GTATCCAGA	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGCCCCCAAGACATATTTTATCTT AAATGTCCAATATCTGCTGATGTGTGTTTGTGCACATTGGGGCCACAGTCIJAATAGGCTAAA AGGCAGTCCCACTGCT
WI-18457	120	T C	---	---	GGTGCTATAGCTGCTGTGTACACCACAAATGGCAGAGGTGAJGTAGAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGTCTATCTCGGGTTTAGGACTCCATTGAG
WI-18462	39	A G	AGAGGTGA	AGATGGTTCT	TGAGGACGTGTGACAAGCTCCAGCAGGGGTGGGGCCGGCTGAGGGTGGGGGTGCGAGGCTJGGT CACTCCCATGTGCCCCCTGGCCGTCCCTCCACTCAACCCACACCTGGCCAGTCCACGTTGAGGT
WI-18476	60	C T	GAGG	GTGACC	

WI-18491	109	G A	A C A A A T G G T A G G T G G T A T T	C G T G T G C A T T T T C T T G T A A T C C	C T A A T G A G A T G A A T A C A T G G A G G C G T T T A G C A G A G T G C C T A A A A C A C A G A T A A G T A A C C A A C A A A T G G T A G G T G G T A T T A A T A C T A T T A T T A T T A A T C C C A G A A T G A C [G/A] G G A T T A C A A G A A A A T G C A C A
EST50757	79	C T	G A G C T C G A G G C T G C T T C T	A C C C T T C A C C C G C C C	A G C C C C C T C C A C T C T G C T T C C A C A A A G T C G G C T C C C G A G A G C T C G A G C T G C T C T C T T T T A T A T G T G C A G G G C C [C/T] G G G C G G G T G A A G G G T C A G A G A
WI-17675	103	T C	G G A C A T T T G G A T G G T G A C T T	G G G G A C C A C C C A G G	G A T C T T G G A A A G C A C T A G A A A C T A A A C A T C T T C A C C A G G T G C T G A A G A A A A G T G C T C T C G T T T A A T T G C C A A G C A G G G A T G T G G A C A T T T G G A T G G T G A C T T T [C/T] C T G G G T G T T C C C C A T A G A T T C A C C A T T G C C T C T A A T G G T G T C T A
WI-16543	67	G T	A G A T A A A C T A C A T T T G G G T T	G A T T C A T C A T T A C A G G G A C T T	G A T C C A T T A C C T A G G T A A A A T T C T C T G A A T G T C A A A C A A A G A G A T A A A C T A C A T T T G G G T T T T G G G T T A A G T C C C C T G T A A T G A T G A A T C A A G A A T C C T C A A G T C T G C T T G C C A C C C A T T T A A T A C G T A T T T T T G T T A A G G C T G A A G T T
WI-17687	107	C G	G C C A A A A A G G T T G G G G A A	T T A C T T T T G T A C C G A C C A G C A	A T C T G A G A T G G A A G A G T T T C A T C C C A A A C C A C T C T C C C C T G A C C C C A G T C C A T G G A A A A A T T G T C T T C C A C A A A A C C G T C C C T G T G T G C C A A A A A G G T T G G G A A [C/G] T G C T G G T G C G G T A C A A A A G T A A T T G
WI-17690b	79	A G	A G G C A T T T T T C T A G C T G T G T T	--- C A A G A G T T A T G G G T C C T G A A T C	A C A A C A T G T G A A A G A A G A T A T G T T G T C T T A C T C A C A G T G G A G G C A T T T T C T A G C T G T T T G A T T G G C T T C C C T A T A G A T T C A G G A C C C A A A C T C T T G T T C T C A C T A C T G C T A T C T G C T A T G C T G A C A A C A T G T G A A A G A A G A T A T G T T G T C T T A C T C A C A G T G G A G G C A T T T T C T A G C T G T T T G A A T T T G G C T T C C C T A T A G A T T C A G G A C C C A A A C T C T T G T T C T C A C T A C T G C T A T G C T A T G C T G C T G
EST51717	128	C T	G C G G A A G A C A G T G A G C T G T T	T T G A G G C A A T A A T C C A G C T C	G A T C C A A T C T C A G T G T C T A A C T A C A T C A T C C C A G A T T A T T [C/T] T G A A G T G G A A C C A C C C T C C G A C C C C A A T G G C A A C A T C A C C C A C T A C C T G G T T T C T G G G A G A G G C A G G C G G A A G A C A G A G T G A G C T G T T C G A G C T G G A T T A T T G C C T C A A A
EST51717	39	C T	--- T G G T C A C T T T G G G G C	--- G G C T C T G C C C A G G C	T T C C A G G T T G A C A G G T T T A T T C A C C C C C T T C C A T C C C C A T G G C C A C C C A G G C A G G A G A C A G G T G T G C T G G A G T C T G G T C A C T T T G G G G C C [C/T] G G C G T G G C A G A G C C C A C T G G G T T A C A T T C T C T G T G G G C A G G T G T G G A C A C
EST53012	97	C T	T G T T G A A A G C A G T C A C A A T G A G T A C	C A T C T G G A T A T C T T G T C A C A T T T T	A A A C T G C A A A T A C A A A A A A C A G A A G T C C A A G A A G G C T A A A G T C T A A G C T A T A A T T A C A C A T G A A G T A T A T G T T G A A A G C A G T C A C A A T G T A C [A/G] A A A A T G T G A C A A G A T A T C C A G A T G T T A A T T T C G A A A T G T C C C A T G A C T T G A C A G A C T G A G A G C C A G C C A G C C A G C C A G G A G A C T G C A G A A C T T A A A C A C [A/G] A G A G A C A T T A T T G T T A G A A A G G C A A G T C T T A C A C T C A A A T A G G T T T T A A C A T G A A C A C A T T A A G G G A G A T G G C C
EST53389	74	A G C A	--- G G A C C T G C A G A A C T T A A A	G C C C T T T C T A A C A A T A A A T G C T C	

[illegible]

[illegible]

TIGR- A003P30	117 C G ---			ACAAGTTCAAAGGAGAACCTTCCTTTGTTTAAATGCAGCTGTGCTCAGAGCCTGTGATTTCCTAGGA AACCATCTGGGTTTAGCCCAATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156 C T A			GCTTGCTTTTATGTTAGGTTCCGGGGAAAGGAGGGCTGACAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGGAGGTTGCAGAACTTCTTTGCTTGGCTAACAGTCTGTCAATGTGACAATAGCCA AACCTCCTCATTCCTATAAA[C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C ---			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTACAGGAAGTACAGGAAGATAAACCAAAATGAT TGAGTATGATAAAGAAATTTGTCATGGCGATT[C/G]AAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTACAGGAAGTACAGGAAGATAAACCAAAATGAT TGA[C/G]ATGATAAAGAAATTTGTCATGGCGATTAAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60 T C GGCATTCTCT			CCTACAATCCTATAATATTGCAAGGGTGGGAAGGATGCAGGAACAGGCATTCTCTTAT[C/G]GCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACCTTTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGCAAAATTTCAAA
TIGR- A004V26	125 A G ---			TCTAGCTATAAGACCAGATTTTAAATTTCTAGATATAGAAATATCCAGAATAATTTCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29 A G CGATCTC			CCAGGCTATAATGTTGTGGGTGGATCT[C/G]GCTCACTGCAACCTCCGCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCAACCCGCCACCTAACTAATTTTGG TATTTTATAGTAGAGACATTGTATTTTATAGTAGACAGG
TIGR- A004X20	25 T C GA			TAAGTTTTCCTTCTCTCTGTAGGAT[C/G]GTCTCCATGTTACAGTCAACTATAAAACATGGCTCATGT TCACTCTGGGCTTCGCTTCAGAGGAGTTGATATTTGGAAGTGGTACCTTTGTTCTGTGTCTTTTCA GACCAACCGCTTCCTTCAATTTCTCAAGGCTTCCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCTCT
TIGR- A004X30	26 T C CCAC			TTTTGAAATCTTAGAGTAGAACCCACT[C/G]ACTCTAGTAATACTTGTATAAAAAATTAATAAGTTT AAACACTTCCATAAAGAATTAGGGTGCCCGCTCTGATTTCCCCCTAGGGATAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAACT			CACGGTATATGCCTTATATATAGGTATATATACAGATCGTACACAATATATTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[C/G]TTGCTTTTCATGAAATTTCTAATTAAAGG ACTGTTGCTTCTTCATATATCAATGGACATTATACAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAGTTATTGGAGGAGCTTGACACCCCTTCTTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTCTCCCGATGACCATCTTTGGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAAGGAAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCG GTGC	GTCTTAGCAGAGGAGATAAATTTGAGGGACAGCCCCAACGGCGCCAGGTAGCCTTCAGGGGGGGCA GGGTGGGGAGGTAGGAGACTCTGGACCGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTC/GTCTAGATTCTTCTGGCCTCTGTGCGAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTC/GTCTAGATTCTTCTGGCCTCTGTGCGAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTTAAAA CTGTTACAC	TTGCTATTAT TTAAGCCCAAC AAAA	CATCAGTAACATATACAAATTTGGTCACTCACTGAACCTTGGCCTCCAATATATTTCTATACAATACTT AACATTATTGAACTTAAACGTGTACACTG/TJTTTGGCTTTAAATAATAGACAATGATTTTGG TCTATTACTTAGTAGACAAAGTGATTACTTTGTAGACAAAGTGATTACTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACCGCCCTCTG/AJCTACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCTGCCATGTGGATAGTACTTTTGCTGCTTGGCCCTACAAAGCCACCTTCTAT TTCATACCAATACCCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAAAACTTTGTTTAGGGAATAAAAAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGAGACAGAATGACCCCTTGGCTCCTTTATTTTCTTTTCAACAGGACC CCACAGATATTGCGGTATGTCATGAGGACTGGGGATGCTCTTCTATTG/CIGGATGCTCTTATTTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGTTACTGCACCTTACAGAG/AJCTCAATTTCCCTGATTAGGA AGCGATGCTAATGGTATTGCATAGGTGTAAGTATAAAATGTTGTTTAAAGAGATCCCAAG CTTGGTATAAGGCAGAAATAAATGGTATAAGGCAGAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	CCCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGCTAAGCACCTACTGCGTATCAGGCACCTGCTGG TGCTTTAC/AJGTACATTACCTCACAGCCAGGGTTGGCAATGGTCATTTTGACAAATGGTCATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAAJCTGTCTTAGGGTGTCTCCCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCTGCTCTCAGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTGTAAAAATCCCCCAAGAGCGCATATGAATCTGCGC

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X57830	106	GC CT	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAATAATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAAGCATATCTGCTGATGCTCATTTTATCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTC
X74070b	72	TG TGGATC	CTTTTAAGAA ATTTTGTTTA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATCTT/GIGATAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTGTGCTTATACACAATTCATCTTTCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	CT ---		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGTCTCATCACCAGCTTJTAGAGCTTCTCCCGAAGGG CCTTAGGATAGGAGAAAGGTTTCATGCACACACGCTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAGTAAGTGAAGG TCCA
D28513b	133	AG ---		---	ATGACCAAAGCCACCACATTTAGAACTTTGGCTGCCCTTGGAAAGTCCAGAGCTGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACCTTTGGACATGGCTCACAAGCAGTTTTTGTATTGACTGCATGAATGCGA GTTGTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	AG ---		---	CCACTCCATCCTGATGCCCAAGTATCCACAGCCTCCTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAAATCTCCAACCTGATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	AG ---		---	CCACTCCATCCTGATGCCCAAGTATCCACAGCCTCCTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAACCTGATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	GA ---		---	CTCCCTGCCTCCTCCTCCTGCTGATGCTCGCTCTCAACAGCCGAAACCTGCTTGAATGGGGG GAGGGGCGTTTC(G/A)CTTCTCCTTCTTCTGGCTTCTCTTATCTTCCACAAACCACTTCTCAATAAA GCCAAAATCTTCTCTTCTCCTCCTCAGGCCACCTCCTGCTCCTCACTCCTGCTGCTGGCTTTT CTGGA
D37931	64	TC ---		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGT/CJ CCCAGGCTGTCTCCTCAGCTCATTTCTCCTACTCTTTTCTCTATATAACTCATTTCTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAATGAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT

D63807	101	C T ---				CAGGAGGACTTCAGTGTGATCCCTGCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGATTTTCTGTTCCAC/C/TAAGAGGAGACTTTTGTTCACAATTGGATCAC AATGCAGAGGAGTCTGTTCTCTCCCGCTGGCTCTCGGTCTGGGAGGGTGACCTGTCCAGATGAC TGGGAACATGCGTGTGACCTC/C/JACAGCTACCTCTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTTCTTAACATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTGAT TTCACAGTGTGTTGATGTTGCTCTGAGAGTCCCTGTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
D90145	21	T C ---				ATTATCACTCTCAAAAATTTGGTGTGTGTTTAAGTACTTCTTATTATGAGCCCT/C/JGAGGA CCAGACATGTTATTATCAAGCCCTTATATACCATCTAAT
EST14035 1a	59	T C ---				GCATTTAAAAATTCACATTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATT ATG/C/JTGTAGATTTTCAGATGTAGGTGCTCAATCTGAGCACTTAICT
EST16668 5	71	C T ---				ACAGACTATCGCCAACTTATAATGCTTAACTTTTATGATCAATAGTAATAATTACA/C/JGAGATA TTCACACTTTATTATAAATAGGGTTTGTGTAAAGATGATTTTCCCAACTGTAGGTTAACAT
EST16904 7	57	C T ---				TTTTTAAGTACCAGAGGCACCTGCTGGAACAGGATGAAACTGATACACC/J/GJTTACTACTTACTC TTCACCTTTCAACCTGATTCCTTAAAGACTTCTACTTAGCAA
EST21863 9	49	A G ---				GGCTGAAGTAGAATCAAGGTTAAGAACATTTTATGCCTTATTCACAAACATTTACTGAGCATA CTAGGTGCTGGGAG/JTGTGACAGTGTGACGCAACAAAAACACAA
EST21885 6	80	G A ---				ATTTAGTGCAAATGACAAAGCCCA/J/GJAGAACAGAGGATCAAAATAGATTGAAATGTATTACC TTCATAAGTATACGAAGTTTAAACAAAGTATGGGAGT
EST22623 8a	26	A G ---				AAAATGATTGAATTCAGGAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTTACAG/J/GJAAATGTGGAAAGATGGCTTTTAAACCC
EST22644 2	98	A G ---				CCTCATTTATTTAAAAAGACGGACATAAAAA/JTATACAAACAAAAAACCCCAAGTCACATTTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST23587 1	31	T A ---				AAAGATCTGGCATTATTCACATCATTCTAAATATTTTGTAAATTTTCCATGAGTATTTTTTCA TGTCACAGCATTTTAACTATCATTTTAGCGTAAATACC/C/JGAATAACCCATAGTTACAGAAATTGG GTCTGTGTAACCTCAAT
EST24246 7	106	T C ---				TAGTTTAAATTTCTGAACCTTTGGCTTATAAAATTTTCTCAACTT/J/GJCATTTAAAAATGTATCAAT GCACCTTCTCAGTAGTACCACATGAAATATAAACCTCGTTC
EST24308 3	45	A G ---				CTTGAACCTTCGGTCTCAAGTGGTACGTCCTCAACCTCCCAAAATGATGGGATTACAGGCATAAG CAGCG/JTGCCTGACCCACATTTCTTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST24435 6	73	G A ---				TATTGTTGCATTATCAAAATGGTTA/J/CJAGTTTTCAATTAACCTGTAATTGATTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAATCGTTAGTTAATGCTACATT
EST25089 6	25	T C ---				

EST25476 9	33 GA ---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAA[G/A]CTTTCTCCTCCTCTAAACCAACACACA AGAGGTCCTCTGCTGCTTTCCACTGAGCTGTGGCGCTGTGGACTTGGACCTGCTGCTGA
EST26183 2	70 TA ---	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACCTTTGTAAGATTGATCTCTAAATAAG ATT[A]ACATTTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 TC ---	---	AGAAATAAGGTGCTACAGAACTCATG[T/C]GATAGCGCTTTCTTTAGGCACATATTATAGCAAT CAGATGAAAGTTCTGTATACACACACACTGTGCCTTAACAACAACACCGTGACTCTGA
EST27816 5a	26 TC ---	---	CAACTCAAGGTACAAGACAATTGCATT[C/T]AACATTGTTATAAATAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 AT ---	---	GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAGGAGGCGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGAT
EST30226 5	25 AC ---	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATAGCTGCATACTAATCTTATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAACAAGACAGACTCATTTCCTTTGA G
EST30935 9a	59 CG ---	---	AGCTATGGTAGAGCAAAATTCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAG[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 GA ---	---	CCGAATATAAGGAAAAAATGGTGG[C/G]ATGCCTCTAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCACTTCTCTATGAATACTGGCAGCTGTTTATTCATGTTTATATGAGTTTCTATGC ATAAAAAATCCAGTAAGA
EST33274 4	27 TC ---	---	TGCTTTGTTCCCTCCAAATCCTAAA[T/C]GTGTGTCTCAAAGAAATTCGTGGAAAGGACTTTGAA TAGAGTTTGTACCATTCAAGTATCTTGAATACAGGTTTCAGATACTATGGAGATGATACCATT GGACTAGGTA
EST33352 7b	75 CG ---	---	TACACATTATCAAGAGACCACTGACATGCATCTCCTCCGCAATACATTCGTCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTTTACTAAGAGATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 AC ---	---	ATTTTCCACAGCAGAGTATTTTATGTGCTGAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAAATGTTCAAAAAGATTACAAATCTCAGTCATTACACACTGAGGCAAC[C/A]AAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 AG ---	---	CCTTTGGGGAGTTTAAAGCCAGATGTGACAAAGTCACTTACAGGAAGACTGGAAATGTAGCCATAG TTGAACCTAACATCGTCTATAG[A/G]ACCAATTTCCCGTCTCCAGTTAGGTTCTAGGCCATACTAAGCT GCTC
EST33508 1b	45 CT ---	---	AAAAACATGCTATTGAACAACTTTTTTATAAGAAATAAGTTGA[C/T]TGAAAAGCAGTTTTTAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---	---	AAAAACATGCTATTTGAACAAACCTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---	---	ACAACATAGGACTGGTTATCTTGTTTGAATAATATGTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAA[C/G]TTCTTGAACTACAGCCTGAATCCCC
EST34739 3	97 T A ---	---	GAAGTATCCCTCCAGTGGCAGAACTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAAACCTC[T/A]GGTGCCTTACAACCTCCAACACTACTGCAGAAATTTCT TGTTGCGCTCATAACA
EST34792 6b	104 A G ---	---	ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGGCACAGATCACGTGGCATCCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTG[A/G]GTATTCAGGAATCTTAGTCCCTATTACA AAGATTTGTTGCTGTG
EST34835 9b	93 T G ---	---	GGAAATGTTCCCTTGCACAAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTCTGCTGTTG[GGCC]TTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---	---	GGAAATGTTCCCTTGCACAAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTG[A/T]GCTTCTGTTGCGCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---	---	CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCTC[G/T]GCGCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---	---	CTTTTCAAATTTTGTAGTGGCATTTAATG[C/T]TATAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTTCCATTTTACTTAGTTCAGAACATTTTCAATTTTCATCT
EST35708 9	32 C T ---	---	CTGCCCCAAATTAACTTTAGGCAATGGAA[C/T]JAGACTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGTTGGCACCTTCTGTTGTG ATGTCAAAGTGTGGCT
EST35747 9	51 C G ---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGAGTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---	---	TGGTCCATTATATAAACTGAGGGAACAAACGGTGTGACATGGCAGACATTTATTTCAATGGAGA AGTTCTCCCATGAACCAAG[A/C]CTTGTCTCATGATAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST36301 4	93 C T ---	---	CACCTGTTTCATTTGTTCACTGGGCTGCTATCTGTGGGCTGATGCTTACCAAGTGTGCTAGCCTACAGC AGTCAGGAGGAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACACAAA
EST36519 0a	33 G T ---	---	GCCATCAGCCCAAGACATGACTACCAACG[C/G]GGCCCCCTGCACCCACTACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGTCTTAGTGT

EST36820 6	50 G A ---	---	GACITATTAGATAAGGGTTTCGGCTACCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAAGG AAGGCTTATTTAAATATGGGAATAAAATACAAAAGGGCCACACCCGATGCAAAAAGACTTT
EST36890 0a	89 C G ---	---	CCTGTGATGTGCATGGGTCCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGATTCCCTA/C/GJAGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 C T ---	---	GAGACAGAAGCCATCAGTTAAATGAGGTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACITTAGCTACCCTGGACAATGCTATCAAGTGTCTGGGAAGGGAG
EST36823 6	103 A T ---	---	ACTGTCTGCCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/TT]CTTTTATGTTCTCCTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	ATGATCGCTTATGTAAITTTGAGGGGCGACATGGGTAAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGTATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	GGTCTACTCTCTTGCCCGAGGACGGTTTGAAACTCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[C/G]GTGAGCCACACACCTGGTCTTGGTTTAAAGTAAACCACTGAA C
EST37269 3b	105 T G ---	---	AATAGTCTATGGCTACGGGCCCCGGGATGTTAAAAATGGGATTTTAAATTAAGATTGTGAACATG CAAAACCCAGCAAAATTTCTCAGCTTATATTTGAAAGT[C/T]G/CAGGAGAAAAATGGGGTCC
EST37284 2	93 G T ---	---	AAAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGAA GCTCTCTGGATAATGTCACTCTAGGA[G/TT]AGTAAACAGGTTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGTGAGGAATA
EST37315 2a	90 A G ---	---	AGATGGGTCTTGTAGCTTGTCTCGGGCTGAACCTAAAGATATCCTCCTGCTCAGCCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACCTT[C/T]AAGGGTGAAGCATACC ATTCCATTTTAGTTGAAATATTCTTCACATAGCCCAACACATTTTTTCAAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	GTGACATCATGTCTCTCAATGCCCTTTCAATTAAATAGATTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTCAAATCACAGTGCTGTGCTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---	---	GTGACATCATGTCTCTCAATGCCCTTTCAATTAAATAGTAGT[C/T]GAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGCTGTGCTCTCAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63	T G	---	---	ACACACAAAAAATGGTGGCAGAAAAATCTGGAAAGATTCTAATAACCTCAATTCTGTGAAAAAC[7]G JAACATGCCTCAAAAAAGAGGGGAAAAAATTTAACAGAAACACGTGCTGACATGATTAGCTT
EST37452 4	46	G A	---	---	AAGACATAAATCTGCAATGAATCAGTTATGAATATTAACCTCT[7]G[A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATCAATGACGTAGAA
EST37613 6	34	A G	---	---	CTAGGCATGGGGCTTTACAGTCATTTATTTACC[A]G[7]GTCATGAATTCATTAAAAACACACGGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAAATCACCCCTGGTTTCATGGATCTTCCATTCTAA
EST38025 4	56	T G	---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTTACATGTTTATATCACTTAT[7]GTTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57	C T	---	---	TCTACCAGGTACCAAAGTATCTGTATATGCTTTAAGTGGCATTTCATGTCACCTTA[7]CJCGCATGG AAGAACGCTCTCCTTTTAAATCCCTAACTCTCTCTTCTGCGGAAGACAGAACGTGCACAA
EST38420 6a	100	T C	---	---	TAAATCAAGGCCCTCTTTTCAATACCAAAACAAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGCATCCTGACTGAQ[7]GTCCTGCAGTGCCCATGGGTCCCGTGCT TATTCATTCTCCTCTCTCA
EST38950 5	25	T C	---	---	TTTATTTGCAAAAGTAAGCAGCCGGT[7]GTCGTCCTGGATTGAGGCTGAGGAAGACATTACTTCTCG CTGGAAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90	T C	---	---	TTTTTGTTACTCTGTAGCCAGTCATTAACTGAAGTTTAAATATATCATTTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATG[7]C[A]AACAAAGTTACTGAATATTTTACCTCGTGGAGTTG
EST39331 1	70	G C	---	---	TCCTTCTGCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAAGACCAGCCATGGAAGGAAAGTA TG[C]G[7]GTTTATAGGGAGAGCTGGCACCCTGGCCTCTAAATCTTCCCTGCCATTGACACAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31	C A	---	---	GTCAACATTGACCTTACATAGTGCCTCTAGT[C]A[7]ACCTATGAGGCACTAGAACCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAATTT
EST40548 4	37	T C	---	---	TTCTAATAGCATGCCCTGTGACAGGGGAACTAAGCTCT[7]CJTCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTTCTCCAGAAAGGCTCAAGGTGTC AATAATCTGTGGGACTCA
EST40549 1	42	A G	---	---	TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCACA[7]G[7]ATAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACACCATTTCTCACTTTGAACCTAGCTCCCTGCAAAGCACCTTCTA CCCTGCACTTTTGGGAG
EST40579 1	81	A C	---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCACTTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAA[A]C[7]GGACTTGGAGACAGCGATTAAATACGGAACAAAGGCTTCCAGGAAG
EST40584 3	68	A G	---	---	TTGTATGGTGTAGGAATTTGGGAAGAAATTTATCTGTGAAGGAAATTTGCCACTGTATGACACACCC A[A]G[7]CTGTACTCCACAATATCCTATGTTTAAAGCT

EST51340	51 G A ---	---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTCGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTCAAACTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTAT
J04162	134 T C ---	---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAAGCTCAGAGCCAGATCCTTTATCCAACTCTCGA T/CJTTCCTTGGTCTCCAGTGGAGGAAAGGCCCATGATCTTCAAGCAGGGAAGCCCAAGTGAGT AGCTG
K01506	63 T C ---	---	---	CTGAAGTCCAGCTGCCCTACAAACTCCATCTCAGCTTTCTCTCAGCTTCTCTCAGTGAACACTACIT/CJC CAGTGGCTGACTGAATTTGCTGACCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCAATCCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTATCCT
L18877	69 T C ---	---	---	TGAGTCTGAGCAGCAGTTGCAGCCAGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAAGGOC CT/CJATCCATTAGTTCCACTGCTGCTGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTCTGTCTATTGGATGACTTTGAGATTATCTTTGTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	---	GCTATTTACATATCCAAAGCCTTTAGGGCTACAGT/CJCTCTTGTCTGACCCCTGTAGGGTGCCA TTTGAGTTTACAGCCTAGAAGAAAGGCTTTGGGCTGTGTGTGGCATAGGCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTTGAGCTCAGGAAGTTGAGACAAACCTGGGCAAT GT
L38517	137 G C ---	---	---	GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCTTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGGCAACACCAAGCGTCCCCCAG CQ/CJCGTGTGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---	---	---	ACTTGAGAAGCAGAGCTGGCCACCTTCTGGAGGCCACTGTGATGATGAGCCCAAGCAATTTGGAGCCA AGTTGAAGGGGACAGGGCAACAAATACAGTAGTAGTTCTTTTGTATTTTGTATATTTGJCGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGGTGGGCTGTGTGCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	---	CAAGTTGTCTCTGCCCATGAGCACACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAAACAGC CCTGTCTCAAAACTGGGTTGCCAGGTCCAATGTACCAGAGCTGGAATCTGAAGCGCTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCTACACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111 TC ---	---	AAGTGAACAGAAAGCAAAGATGGATTGTTCCTATAAAGCACATAGTATGTTTACTGGTATCGT AAGAAAGCTGGAAGAAGAGCTCAAGTTTTGGTTTACTTTTTCAGAAAT/CJGAAGAAGTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTGTAGCCCAATGCTCCAAAAGCTCATCTGTACCTTGGAGATCCA GTC
M18079	52 GA ---	---	GCGCACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTTATTTCACC CCATCAAGTATAAGGTTACTGATTGATTGGTCCCTTTTATAAACATTGGTATATTCCATTATGCCAA AGCAAAAAGAAAGTAAAGCTAA
M19169	113 TC ---	---	TAGGGATCTGTGCCAGGCCATTGGACCCAGCCACACCCACTCCACCCCTGTAGTCTCCACCC TGGACTGGTGGCCCCACCCCTGCGGGAGGCCCTCCCATGTGCTGTC/CJGCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCCTTTGTTGCTCAGCAGGGCGCTCCGCCCTCCCTCTCTCTGCTTCTAATA GC
M21539	114 TG ---	---	TCACCTCGTTCCACAGCTCCACCTGCATCTTCTCATCAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTTAGCCTGATCTGCCCATGATGATCCCGACAGCAAAAT/GJGTTTCTCTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 AG ---	---	CCTAGCATATTCTGCCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGACTTC CTGATTTTCTTTCTCAAGTGTTACCTACTAAG[G/A]GATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 AG ---	---	CCTAGCATATTCTGCCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGACTTC CTGATTTTCTTTCTCTCA/GJGTTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 CG ---	---	CCTAGCATATTCTGCCCCCATTTATCATATCCCTTTTCTCCTCTC/CJCAAAATGTTTCTCCTCTCAC TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGACTTC TTCCTGATTTTCTTTCTCTCAAGTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 GC ---	---	TAAGGACGTGTGAGGGAGGCCAGTCACAGTCAGCAATCCACAACCCACTTGAC[G/C]AATGCT TGCCAAAGCTGTTTAAAGCCAAAGAACACCCCTTCTTTGTTCCAAATTAACCTTAGAAGAAACCCCA CAATAAAGCAATTCAATC
M81695	34 GA ---	---	ACTTACTACCCCTACCTGTGAGGCTGACGGGG[G/A]GAACCACTGCACCCAGAGAGGCTGGG ATGGGCTGCTCTGCTTTGGGAGAAAACGCTTCTGTTGGGAAGGGCTTGTCTTGCAAGGTTT CAACTGGAAACCCCTAGGACAGGGTCCCTGCTGTGTTCCCCCAAAAGGACTTGACTTGCAATTCTACC T

U06641d	166 C T ---	---	CTCCTCCTTTATTTAGCATGGAGGTTTAAATGGAGGATCTCCTTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAAATTTAAAAAGATCTTTTACAACTTACCTTGTAAAGACAAATTT TATTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAATTTCTATGTCAATGATTTTAAAGCTA TGAAATACAATGGGGGA
U09607	39 T C ---	---	GAGGCCCTATGAGGGTCTCTACTTCAGGAACACCCCA[T/C]GACATTGCATTTGGGGGGCTCCCG TGGCCTGTAGAATAGCCTGTGGCCTTTGCAATTTGTAAGTTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTGGCCCAAGGAAGCAAGCAACCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATTCAAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[T/C]ACATCTGCCGCCCTTCAGGCCCTCCCAAGCCCTCCTCTTGTCTTC ATTCAATCAACAAAATTTGGC
U10694	20 C G ---	---	GTGACATGAGGCCCATCTT[C/G]GCTGTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCACTCTCTGGTTCCCTGTCTATTTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATTTCAAAATGTTCTTTTAAATGGTCAGTTTAAATGAACCTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGACAAAGTTGTTTAAAC CTCTTTGTTGAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCCAAGAGAT[T/C]TTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187 T C ---	---	TTTCTGCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGGAAAGATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATGT[C/T]TGGTCTCATAC CTCATATGCAGGATTCAATCA
U17077	122 T C ---	---	TCCAATTTATGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAACAGAACGTCCTTGGAGACTGAGCGATGACACCACACT[C/T]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAACAACTGTCTCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAATAGACTCAGCTATGTCCTGATTCAGCTGGGTAGTTCTAGAACTT[C/G]JAGAAG CTCCATCTTTTAAATGTTTTTATTTGTTATGTCCTCCCTCCCGGCTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACCTTCC AAGCTTTAGTAGAGAGAGCC

U25975b	164	C A	---	---	---	TCACCTGCTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAAAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAC/C/AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143	C G	---	---	---	TCACCTGCTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAAAATGACTATTCTCTG AAGACAAC/C/G/AAGAGAAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61	A G	---	---	---	CAGGGAGAGGTTATTACAAACCTCACAAACTAGTATCATTTTAGGGGTGTTGACACACCA/A/GJTT TTGAGTGTAAGTGGCTGTTGATTTTAAAGTAGTTCTATTTTCTATCCCTTAAAGAAAAATT GCATGAAACTAGGCTTCTGTAACTCAATATCCCAACATTTCTGCAATGGCAGCATTTCCGACCAACAAAA TCC
U28413	29	C T	---	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/JGGGTAATATTTTCTCATGTTTAAAAATGAGGTT AATATTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTTGCTACAGTACAAGTAAACACAAGTCGTTGTACCTCAGTT G
U30884c	89	A G	---	---	---	TAGGGTAGCATTTAAGATTGAGGAGTCATTAGCAGTGATGATTTTGGACCTGCCGTATAATCTGTT CTTCTATTCCACGTTAGCCA/A/GJTTGTTCTTGATGAATCTATATGATCATAAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAGT GCTGTCA
U30884a	34	A G	---	---	---	TAGGGTAGCATTTAAGATTGAGGAGTCATTAGC/A/GJTGATGATTTTGGACCTGCCGTATAATCT GTTCTTTATCCACGTTAGCCAATTTGTTCTTGATGAATCTATATGATCATAAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAGT GCTGTCA
U31216b	78	A G	---	---	---	GGGACAGCATATGTGGCACCCGCTCTCTGTGACGTGAAGACCAATGAGACGGCTGCAACCAACA GCCGTATCAA/A/GJCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTACAACGTAGAGAGGAGGAGGATGCCAGCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A	---	---	---	GGGACAGCATATGTGGCACCCGCTCTCTGTGACGTGAAGACCAATGAGACGGCTGCAACCAACA GCC/G/ATCATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTACAACGTAGAGAGGAGGAGGATGCCAGCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	76 GA ---	---	AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTCTGTTACAAATGCTAGGTCCACCTGCCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTTCCTCATTTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 CT ---	---	AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCAGCCCAAAATCTGGTGCCTCTCTCTGTTACAAATGCTAGGTCCACCTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCCTCATTTCACTTGACCCCTGCCACCTCTCC ACCTAACTGGCTTACTTCCT
U37519a	78 CT ---	---	ACGGGTACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCACTCACATTGTTCTCC AGACCGCAGG[C/T]TCCCGAGCTCAGGTGCTGGAGCTGCACATGACTGCATCCTGCTGCCAGG GCTGCAAGCAAGTCTTGCTTCTATCTGGGGACGCTGCTCGAGAGAGCGCGAGAGCGCGCAGAAC ATGCCAGGTGTC
U37690	54 AG ---	---	GACCAGCTGAACCCACCCACCCGCTGCTGACTGACCATGGCCCTGAGCGTCC[T/G]CCCCGAATTC ACGAGGCTGAGGCATCCGGAGCTGGCGTAATGCCCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAGGTCTTT
V00540	39 TC ---	---	TGAAACCGTTCAACATGGAATGATCTGTTGACTAAT[C/J]ACACCAGTCCACACTTCTATGACT TCTGCCATTCAAAGACTCATTTCTCTATAACCCAGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGAAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 AT ---	---	TCAAGAAAGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACCTGAGCCTCTCTGAGACCCTGTTTAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTCCAGTAGCTAAGACCCTAGAAATTTGGATTCTCTGTTTTTTCATGCTCTCCTT GTAAACCCTGAGATCATCAG
X52011b	148 CT ---	---	AGGAAGATCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAGTTGCGAAATTCGG AAATCTGTTGTGCA[C/T]GCTCAATGAAACGCCCTTTGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 AC ---	---	AGGAAGATCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAA[A/C]GTTCGAAATTT GCGAAATCTGTTGTGCACGCTCAATGAAACGCCCTTCGGCTTTTGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT

X54741	24 A G ---	---	---	CAGGCCACCTGTCTCTCTCCACAG/GTGCACAGCTTCTCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GGACAAATGGAATCCCGAGGCTCCAGGACTGGGCTTGCCAGGCTTGCAATAGCAAGGCCAG GGCAGCTGGAGACGATCTTGCTGGCAGGCTGGCTTGCCAGCCACCTGGCCCCCTTCTCC
				AGCAAGCAGTGC
X54869	99 A G ---	---	---	AAGCATTTGCGTTTACAGTGATCAGATACATTTATTTCTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATTTATTTGCTCTG/GATACAAAAATCTAAATCAATTTATTGAAATAG GATGCACACAATTTACTAAAGTACAGACATCTAGCATTTGTGCGGCTCATTTTGTCTCAACATGGTA
X86924	147 G A ---	---	---	GCGGTGCTGACACCTCCAGAACGAGGTGCTGGGCGCGTCTGCGTGGACCCCGGGAACCTCTC CTGCCGGAAGCGGACGGAGGATGGCCCCAACTTGGCTGCCACTTGACTTACCAAAATCCCT TCCTGGAGACT/G/AACCTGGTGTCTCAGGAGCGAAGGACTGTGAACITTTGGGCTGAAGAGCCAGA
				GAAATGTGAAGAAATGTGACAAAGCCTTTAAGCGGTTGTACACTTGATTGTATATAGATAAT/GIT CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAAGCATTTAATTAATCTCATACCTTA TTGCACAGGAAGCATTTATCTTGAGAAAAATTTGATAAAGAAATGGAAGTCAATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X78932	62 T G ---	---	---	CTCAACCCATAACCTCAACACATCT/GTATCTCCACCCACATCCACACCATCCACCTCCATCC CCAAACCATCTCATCCCCAACTACAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCAGGGCCATCCCCAAACCCATCCCCAAGCC AAACTCAACACCATCC
X80026	25 T C ---	---	---	ACCCCACTCAAGTCCAGGCCCGGCGATCTTCTGCGCTGCTTGTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTGTCTAGCTACTTCTCTG/GCAGCTTTGAAAGACCCCTCCCACTCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197b	99 G C ---	---	---	ACCCCACTCAAGTCCAGGCCCGGCG/GGCTTTCTGCGCTGCTTGTGGCCCATCCAGTCC AGGCGCTGGAGCAAGTGTCTAGCTACTTCTCTGCACTTTGAAAGACCCCTCCCACTCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28 A G ---	---	---	GGCACCCAGAGTGACACAAGTCCAGAGGGAGCGCGCGCTCGCGGTGTCGGTTCCTTTT CAGCCCCGGAGAGTCTGACCTGGGGCTTCTCAAGCTCACTGGGACAGCTCCCGCGGCTCT CTTTCTCCCAAGC/G/AJAAACCAATGCGCCCCCTTCACTCGCGTGGCGGAGCGCGGGGCTT CTTCAGAGC
X85106	150 G A ---	---	---	ACCACAGCCATGGTCTAAGGACATGATCGGGTGCCCGACAGCGTGTGCACAGGGGACCCCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCT/GJGGG ATGCGCAGGAGGAGCCATCGGGTACTACGAGCAACACTCACTGTCAGGCTGAGATAAATCCC GGGA
X87160	128 T G ---	---	---	

X87344	34 C T ---	---	CATCCCAAGGCACCTGGTGTGACTCTGCTTCTGTC/TACTACCCAGAGCCTCTGCCTGTGCACTGC AAGCTGTGTCTACTCAGGCCCCCAAGGGACTCTCTGTTTCCATTCTCCCCACAGACCTGTCAAGAG AAGCATGACAAACAAATCATTTACCGACTTTAGTGCTTTTTT
X87838	179 G T ---	---	GGTGGCTGGTATCTCAGAAAGTGCCTGACACACTACCAAGCTGAGTTTCTATGGGAACAATTGA AGTAAACTTTTGTCTGCTCTTTTGGTCGAGGAGTAACAATACAAATGGATTTTGGGAGTGACTC AAGAAGTGAAGAATGCACAAGAATGGATCACAAGATGGAATTGA/GTCAAACCCCTAGCCTTGCTT GTTAAATTT
Z14138	81 A G ---	---	GTTCTGCTGCCTTACACAGGGGCCCTGTACAGTGAATGGTGCCATTTTCGAAGGAGCAGCAGTGTGA CCTCCTGTGACCC/GTGAATGTGCCTCCAGCGGCCCTGTGTTTGACATGTGAAGCTATTGTGAT ATGCACAGGTCTCAAGGTTCTCATTTCTCAGGTGACGTGATTTCTAAGGCAGGATTTGAGAGTTCACA GAAGGAT
Z18859	191 A C ---	---	TAATCCTCACCATTCTCAGGTATAAGTTCTATAACAGGCTTGGAATCTGGGTAATTAACAAACAGA AAATTATAGTCAATATACCATGACATGAAGAATGAATCCATTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC/ACJ/CAGGTTTC CAGTACTGGTTTCCAA
Z23091	159 G A ---	---	AGAACCTGACACAGATGTGGCTGGAGGGGAATCCAGACCCGCTGCTGCTCTCCTCCCTCCCTCCCTCC CACTCCTCCTCTCTCTCTCTCTCTCACTGCCACGCCCTCTCTTCCCTCCTCCTCCCTCCCTCCCTCCG CTCTGTGCTCTTCATTCTCAQ/GAGCCCCGCAACCCCTCTCTCTCTGTCCTCCCGCCGCTCTCTGGAAA CTGAGCTTGACGTTTG
11595b	125 A G ---	---	GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAACCTGACCCTAGTTGTGCTCCAGGACCTA/GJ/GCGTGC TCACCTACCTTGCTTTGTGTGAAGGAGTGTTTCCCATGACTGTTTAAGTGACAAGTGCCATGG ATATCTACACCCGTCAACAGACTAGATTGTCTCAATGTCTTGGCTTGGAC
11595	125 A G ---	---	GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAACCTGACCCTAGTTGTGCTCCAGGACCTA/GJ/GCGTGC TCACCTACCTTGCTTTGTGTGAAGGAGTGTTTCCCATGACTGTTTAAGTGACAAGTGCCATGG ATATCTACACCGTCAACAGACTAGATTGTCTCAATGTCTTGGCTTGGAC
1241	131 G T ---	---	TATATCACATTAGTATGTCACCTGCCATGGTAAGGACTTTGATCAGTGGAAATAAGAACACTTTTGAA TGCTCTGTCTCTTTCAATAAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCACTTGT JGCAGGAGTGTTTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAAGTAGCAATGGGA ATGAAATAGGAGGCCCTGAGATCCACTGGATAATCTATAAAACCAAGAGAAAG

1282	130 CT ---	---	GTGCGATCACCCTACAGTCTAATTTTCAGATGTTTTCATTAACCCCTAAAGAAATCTTGTACCCATTAGCAATTAATCTCATTCTGCCCTCACCAGGCTACTCTTTATCGCTATAGATTTGCCQ[C]/TACTTGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTCTCTTCACTGAGAATAATGTTTCAAGGT
6810	68 CT ---	---	AGTATCACACATACTTAATATATAGATATACACAATAATAAAATCACTCCCTAGCTTGAAAACCTTTA/C/JAGAAGCATTTTAAATTTTACAACACAAGCTCAACGAACTTACAAATAGTCTAGTAGTCTGTTACGTGCCAAGGATAAGGCTGAACAATAAATTAACCTTTAAATGTCTATGAACAAGTACAAATTTCTTTTGTAGTTCTGCAGAGCAATGACCCTAAGAAATATTTTAAAGGC
6817	118 AC ---	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC/JC/JGTGGATACCCCTGTGCTCTACTGGCCTCCAAAGGCATTGAGGGATCATCAAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAAGGTGCGGCTGTGCAGATCGGCTTTTGGTTGTTGCTTAG
6819b	212 C ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGAGGAGCCTAGTAAAGCCCCGTCAGTAGTACACATTTCTGTATGGTCTTCAACAGTTTTCATATACAAAATTTCTGCTATTTTGTCTTTAGCAAAACAGCAATAACTTTTGTGTTCCCTATATGACACCTAATATCCA
6819a	166 GT ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGAGGAGCCTAGTAAAGCCCCGTCAGTAGTACACATTTCTGTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTTAGCAAAACAGCAATAACTTTTGTGTTCCCTATATGACACCTAATATCCA
681xx	39 AG ---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT/JG/JTTATACTATGGCACCATTGGGACACAGATTATATGTCAGACACCCAGCAATGTCCCTTAAGATATGCAGCAAGCACAAATCTGTCTATGTTTAAACAAAAGAAATGAACGCTAGG
6972b	149 GT ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAAACTATTGATTATGGCACAAATTCAGAG/JC/JCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGAGAGTGTATGTGTCAGGAAT
6972a	122 AG ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAA/JG/JCTATTGATTATGCCACAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGAGAGTGTATGTGTCAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAAATTAATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCGTATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGCAGAC/C/
7598j	208 A T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAAATTAATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCGTATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGCAT/T/GA
7598l	192 G T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAAATTAATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCGTATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAAATTAATTTCTTGAGGATGCCTTTTA ATATTTGATCC/C/T/ATTTATGTGAGAGATTTTCCGTATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAAATTAATTTCTTGAGGATGCCTTTTA ATATTTGAT/C/T/CCATTATGTGAGAGATTTTCCGTATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAAATTAATTTCTTGAGGATGCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCGTATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA/C/T/AGATTTTACCTGGAGAAATGAAAATTAATTTCTTGAGGATGCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCGTATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGC/C/T/GCTAACAGATTTTACCTGGAGAAATGAAAATTAATTTCTTGAGGATGCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCGTATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---			AAAGGTAAATCAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA/GJAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTTATCTTGAGGATGCCTT TTAATATTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---			AAAGGTAAATCAAGTTCCTCTATAAATTATGATTTACAAAAGACAC/GJCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTTATCTTGAGGATGCCTT TTAATATTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---			AAAGGTAAATCAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAAATTTATCTTGAGGATGCCTT TTAATATTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---			GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTAGACATCTTGCCAGCTCTCCTGTA ATACITTAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAA/TTCCTTGAGGTTCCCT
7998b	94 A C ---			GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTAGACATCTTGCCAGCTCTCCTGTA ATACITTAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAA/TTCCTTGAGGTTCCCT
7998a	75 A T ---			GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTAGACATCTTGCCAGCTCTCCTGTA ATACITTAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAA/TTCCTTGAGGTTCCCT
8071	119 A G ---			AAATACAGAAATTTATTTAGAAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAATGGGTTCCCAATAAATGGAATTTTAGGGCAACAAAGTCTAAAAGGCC/GJCAAAAAGAGA AATAGCACCACGTGCTATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGAAATCCACACAGAGCATGCACACATTTTATCAT
8467b	93 C T ---			AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA/C/TJGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCATAAGCTTGCAAAAAGTATTAAGGAAAAATTAATG
8467a	70 A G ---			AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG/GJCGCAAAATCCACTTTGCTGTAAACGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCATAAGCTTGCAAAAAGTATTAAGGAAAAATTAATG
8498	84 C T ---			AGGTTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG/C/TJAACTTCAATTAATCGAAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTCTCTCAATACAGAACCAAGGAATGTAATTTTCTTAACCTCAG

WI-18562	29 GA ---	---	---	CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATCTTACATTT TAGCATTAATCAGAAACGA
WI-18618	51 AC ---	---	---	ATAGCAGACTTTTAAATCAATGCCAGACAAAAGTGAGCGGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGTATAATTTGTAACACAGTGCTCGCACAGTTC AC
WI-18683	22 CT ---	---	---	TAAGCTGTTGAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCCAAAGCCTGCCTGCAGT
WI-18520	75 GA ---	---	---	GACTTTGGTGATTTAATTGCTTTCCCTTAAATATAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAATACTACTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCTCTCTTCCGTGAGAC
WI-18553	94 AG ---	---	---	AAATAAGTTTTATTGGCACACAGCCAAAGCCCACTGGATGACACATTTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]ACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69 TA ---	---	---	GTCTATTTCAAATTAGCTAGACCCATTTCATTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTTAAATCAGTGCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94 GA ---	---	---	AACITTTATTGATCTGACGATCAGGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAAACAAAG[A/G]ATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71 TC ---	---	---	AACITTTATTGATCTGACGATCAGGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96 AG ---	---	---	AACITTTATTGATCTGACGATCAGGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAAACCAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44 GA ---	---	---	TTTATTACAATATTAGGTGGCACATAACTAACAAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCA TAGACTTTGCAACTCAGCCAGAAGTAAACTCGAATA
WI-18715	76 GA ---	---	---	TTATTACAAAAAGTGATATTGCAGAGGCTCTGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGAGCCTCCAGGTGGAAGGGTATTTTTTAATAAAAAATAA TGGAGCTACAACACCCCCC
WI-18535	107 GA ---	---	---	GTAAATAAGTTTTATTGGCACAGCCACGCTCGTTTCATTCATATGCCATTGACATCTGCTGTTCOCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGGTCCCGGTG
D17525	107 CT ---	---	---	AGAGTGGTGCAGAACACAGCCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTCGAACCTTCAGTTCTTCATAAGATGGAAG[C/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAATGCACCTTAGCAGAGGTGATGTGTCTACCGAGCAGCAAG

DWU-133c	313 A G ---	---	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGTCTCATGACITTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAATATTTTGTGGGAGTCCT GATTTAAACTAAGACTGGCTTGGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236 T C ---	---	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGTCTCATGACITTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAATATTTTGTGGGAGTCCT GATTTAAACTAAGACTGGCTTGGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199 C T ---	---	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGTCTCATGACITTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAATATTTTGTGGGAGTCCT GATTTAAACTAAGACTGGCTTGGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC TCCAAATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102 C T ---	---	ATGAGATCCTTTAAATCCTTCATGAACGTTTGTGGTGGCACCTCCTACGTCAAACATGAAGTG TGTTCCCTTCAGTGCATCTGGGAAGATTTCTACCCCTGACCAACAGTTCCTTCAGCTTCCATTCGCC CCTCATTTATCCCTCAACCCCGACGCCACAGGTTTATACAGCTCAGCTTTTGCTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAGGATTCATGTGGAATATAAAGAT
DWU-387	169 G T ---	---	GTGTATAAAATGCAACTGTTGATTTCTCAACATGGCTCACAAATTTCTATCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTAAACTGCACTGCCAACAGTTCACCTCATATATAAAGCATTATTTTAA CTCTTTTGAGGTGAATATAATTTATATTACAATGCTTAAAGCTTCTTTAACTAAGTATTTTCA GGTCTCACCAAGTATCAAAAGTAATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172 -- ---	---	ATTTAGTGTCTTGGTTAAAAATCATTTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCAATTTAAATCACTGTAAATTAATAGTTTGTATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTCAATTTTGTCTTAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTCTGTTAG GCCCTTCTTCTTACAAATGAAGAGATGATCTTCTAGTTTATGGTTA
DWU-447	85 A G ---	---	ATTTAGTGTCTTGGTTAAAAATCATTTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCAATTTAAAGTACACTGTAAATTAATAGTTTGTATTAGAGCACAAAGCTTAGCTAAT CAACCATTTATTTTCAATTTTGTCTTAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTCTG TTAGGCCCTTCTTCTTACAAATGAAGAGATGATCTTCTAGTTTATGGTTA
DWU-478	63 C G ---	---	GTAAATTCAGTTTTTTCCAGTTCCTCTTTTGTGCTGCTTCTCAATAGCGTTTAAAGGTGAGTGGAT AAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGTTTCTTCATGAGTAGTGGCTATGCA GGAGCTTCTGGGAGATTTTTTT

DWU-505	67 A T ---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCTCATACAGAAAAATCTATCACCATACAAAAATTA[A/T]TGCAATTTATGTTTAAAGCACAGGTGTACCGAAACTGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCAATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACITTTGACTTTGAGCTTTAAACITTTAA
DWU-512	131 A G ---	---	AAAATCCAGGCATTTGAAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAGATGGAGAAAGGTGAACCTGCTTTGAATATCCAGATGTTTGGTC[A/G] TGCATATGCCAGTGAGCAGGTATGTTTGCCTTTGCTTGCACTGAAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTTTATCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	AACTGCATATAGATAATTATCCAGGATGTGGCTCATCTTTTCAGCTTGTTTCTATACTGTTGTA ATATACAGTTTTTGTAAACCATATGATTGA[C/A]AAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAATAACATATCTTCTGCTTTTCAAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAACTCTAAAAATCTAGTCTCTGATTTGC
DWU-59	94 C T ---	---	CATTTCTTTGTGAAGGTAATGGACTCACAAGGGGGAAGAACATGCTGAGATGGAAAGTCTACCGG CCCTTTCTTTGTGAACGTCACATTTGGC[C/T]GAGCCGTGTTTCCAGGTGCCAGACTCGTTTTTG GTAGTTGTTTTAACTTCCAAGTGGTTTTACTTCTGATAGCCCGTGATTTTCCCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTAGTGGTTAAGC
EST11	68 C -- ---	---	CTTGATCATGGGTGGAATTTTGTGATCTGGGCTTCATGGGATGCATAAAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	CACACTGGCATCTAGGCCCTTCGCTGCATTGCAAGAGGAGAGCAGGTCCCTCCTGGAGAA[C/T]G CTCGTTCCCGAGCCCAACCGGCTTTGCACACACAGGCTGTTGAGGCAGGAGGTGGTGAAGACGT AGCTGTAGACCCCAAGCAACCAAGCCCTGGGACCCCTGCGGGAGAGGAGCAGCTTTAGAACATGGAA AAGTGGTGCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGCTGTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAAATCTTTTCAATA[A/T]A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT[C/A]AACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	TGTAAGGTGACTTCTATAAGCTTCTTAACTGTCAAACTTTCAATTTACTGAGATTATTTACAGGCCAAT GTGTC[CT]TTGGGTCTGAGATTGATTATCAGCTGGGTAAAGTTAACTGTTCTCTGTTTCA

WI-18063	105 GA ---	---	---	AGGCTTTAAACTGATAACAAATTTGCCCTTTAATCACAATACAAAACCTCTGCACCTTTTCATCTCCTTC CCATGTTTCTGATTTTGATGTAACCTTAAATTTGTTG[A]TCCCTTTAACAAATATACTGTAGCTGCA
WI-18078	86 AT ---	---	---	AGTTGAAAGATCAGAGAGGTTATGTTGGTAGTAGTGAACCTCAGATTCAAACCTGGTCCAGTGTG TTGTTTTTTCAGCATCAGATGTCCACTAGCCAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90 TC ---	---	---	CCAAAGCTCACTCAGTATTTAATCATCTGCTAAATTTTCATCTTTTAAATCCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACITTC[GGGCCCTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18119	38 TC ---	---	---	GCAATCTGTAACAGTTTTGGTAGTGGTATTACAGAGGATTCITTGTAATGGATTGGAGTACTTAC CACTATTTTCATCTGCTGCTGAATAGTTCACTAACCAACTACTGACAACAGTTTAATTTGGTCTT
WI-18142	66 TG ---	---	---	TTCAAGATAATTACAATTTGGAAGGGGACCAATAATTCACITTTTAAATCGAAAAATAATCTATATAC T/GCCCAATAAAGCTACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA
WI-18178	68 TC ---	---	---	GCATAGGTTGAGGGGTGTACAAGAGGAGAACAGATTCACTCCATGCTGAGGTTAGTCTGGGG GT/CJCGCGGGATGGACACAGACAGACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35 GT ---	---	---	TCAATCTGAAACTTGTGTAGCCAGCATGGGGTGTGGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACACAGTACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115 GA ---	---	---	ACAGATGTCAGTTGTTGAATGGCCCATTAAGATATGGGGCTTTCTGTTAAAAGTCATCCAAA AGGCTTGGCAAGAGTTTGCTATACAACGGAGGGACAGAGAACATGA[G]A]CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18261	26 GA ---	---	---	GATTTGAAGGGATGCTTTTAACTG[A]TGAAAAGCGTGATAGAGGAACTGTTTAAGATAAACAA CTTATAAATACTCCCAATTGTAGAAGTGAAGATTG
WI-18268	88 CT ---	---	---	TAGGAGGAAAGGAGGTGGCTGCCCTGGCCCTCAAGACATGAGAACGGGTGGTGGCTTCCAAGC TTCTTACTTCCCCATAGATTC]CCTGACAATGTCTGCAGAAGCCTCCAACCTGGAAC
WI-18299f	107 CA ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTTGCCAAATTTT ATCTATTTGGGCTGAGAATTCACAAATTTGA[G]GAATCTTTTGCCAATTTTGACATATCTG CAG
WI-18299e	101 AG ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTTGCCAAATTTT ATCTATTTG[G]A]GTCTGAGAATTCACAAATTTGAAGAATCTTTTGCCAATTTTGACATATCTG CAG
WI-18299d	77 GA ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTTGCCAAATTTT T/G]ATCTATTTGGGCTGAGAATTCACAAATTTGAAGAATTTCTTTTGCCAATTTTGACATATCTG CAG
WI-18299c	67 TG ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTTGCCAAATTTT T/G]ATCTATTTGGGCTGAGAATTCACAAATTTGAAGAATTTCTTTTGCCAATTTTGACATATCTG CAG

WI-18299b	52 GA ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTG[G/A]TTTGCCAAATTTT TTTATCTATTGGGCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18299a	48 CT ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAA[C/T]TTGGTTTGCCAAATTTT TTTATCTATTGGGCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18307	76 GA ---	---	---	TCAACTTGTACCAAGTTTAGCAGCAAGAGGATACCTCTCTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAAGCATCCAGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72 CT ---	---	---	TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAACTCCGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48 TC ---	---	---	ATGAAAGTCACCTTCAATCATAGGGTCAAGAGAAAGAATGTTTTCAGAT[C/T]TAATCTATGAAAA GGTGTATCTGCTTGCAATTTAAGAAACAACAAGTCA
WI-18395	77 GC ---	---	---	TCCTGACATGATCTGTGAAATAACGTGATTGTGGTTGAAATTTCTGGAAAAATTTGAAGAAATAAATTG ATTATTCAAAG[G/C]TGTGCATGGTTTATACATACTCTCTCTCTTAATGCAAGCTATG
WI-18398	62 GT ---	---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAGAAAGAAACAACTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCATTAATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18398	21 CA ---	---	---	CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTTTCGCTCTTTCTTAAATTTAAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCAACTTGACAAAGTC AATGAAAA
WI-18409a	20 CA ---	---	---	AAGATGGGAAAGAGGAAATC[C/A]TTTTTCTTACTAGAGATTTTTTCCCTTTAATCCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAAAGCTCTGGGGCCCAAGAGGCCCAAGTGCTA
WI-18442	62 CT ---	---	---	AAAAGGAAAGAAAGGATGGAGTAAGAGAGAGAGAGAGAGAGAGGAAACAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGGAACACACAGAGAAAAAAGG TTTATAGTGGGAGAGAGGA
WI-18452	38 GA ---	---	---	TTGATGTTAATACTGTCACTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCCTCATATTTTCCAAACCA
WI-18489	102 AC ---	---	---	ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTTGAAAGAGAGAGATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
EST5b	93 A ---	---	---	CTGGTGGGAGGAAACAAATTTGTGGTATATTATCATCAATGGAAAACTCTTCAGAAATAAGAAAGGAA CAAACCACTGAATCACACAACATGGACAAATCTCAATCATATTGCTGTGATGGAAAGAAACCAATTCA TAAGAATACACAGTACAT

EST5	93 A ---	---	CTGGTGGGAGGAAACAAATTTGGGTATATTCATACAATGGAAACTCTTCAGAAATTAAGAAGGAA CAAACTGAAATCACAAACATGGACAAATCTCAAATCATTTATGCTGATGGAAGAAACCACTTCA TAAGAATACACAGTACAT
EST6	48 C ---	---	TTAGCTACTTTTTCAGAAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAGCTTTTCTTCTTTTGAACAAGACAAAGCAAGCCACATTTTGCATTAGACAGAT
EST8	158 A ---	---	GGACAGGACCTCTATTCOCGCTGTGCAGCAGCGGCTGATGGACTGAGGCCCGCAGGGATCTGGGCC CTCTCTCAGGGCGTCTCAGGACCCAGAGCTGTCTCTGCTTTGAGTTCCCTAGAGCTGTGGGCCA GATAGCTTCTGAGTTGCAAGCAGATGGAGATTGGACACTGTGTCTTTGGTGGGT
WI-18740c	104 GT ---	---	TCCTCATTGTGGGATGATGAGAAGAAATGATTGGGAAAATTAAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTACCATCATGTATCCAGTAGTG[GT/TAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18740b	96 C G ---	---	TCCTCATTGTGGGATGATGAGAAGAAATGATTGGGAAAATTAAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTACCATCATGTATC[GT/AGTAGTGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18985a	105 CT ---	---	CCAAAGTCTCTGCTCATAAAGAGTTTTGGGATGGGAGAGATCCAGACCATCTTGGGGCA GCCAGGCCCTGCCCTTCAATTTACAGAGGTAGCACA[GT/TTGATTCACACAAAACCCCTTCCCC TTTTAAATGATTCTGTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTTCTCTT TGAAGCAATGACAAGCATTACTTTCACGGTGGTTTTGTTTTCTTAT
WI-18746	114 GA ---	---	GCCAGCAGCTGAAGTCTTTTCTCTCTCCTCGGCTGGAGAACATCAAGATACCTTTGCGTGGATCA AGCTGTGACTTGACCGTTTTATATTACTTTTGTAAATATCTT[GT/ATCCACATTCTACTCAGCT TTGGATGTGGTTACCG
WI-19112	212 GA ---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGTATCTCATGACAAACACAAAGAACCCGAGACAAA TCTTTGCGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTTAAAGAACACCGGTGATATCTTTGAG GGTGACAAGGC[GT/ATCTCTTCAACAGTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 AC ---	---	TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTTCTAGATCATGT CTCAATGGAAACACTCTTCTTTAGCCTTACTTGAATCTTGCCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGTCTTTGATTAAACTGAAATTTT TTTTAAGCTAACAAAGATCATAATTTT[GT/ATGATTAGCCGTGTAAC
WI-19057	175 GA ---	---	CCCATTATTATAGCCAGTGTCTCAAAGAGTAGAGGCGTCTACTGGTCTTCAACTCTTCA GTCTTCTGACGGCGACTTACCGTGACAGCGGAAGTGTATTGTAGTCCAGGCAACCGCAGCCACTG TCTTCATGCAGGAACACAGTGCCAGATCCCCACAGCTC[GT/ATCTCTTCTATCTTGGTTTTGCGACA

WI-20103	168	CT ---	---	TGGGACTCCAACTCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGTCTCCCA(C/J)TTCATTCGTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	GA ---	---	GGCTTACCACTTTGCACATATACATATGCACCACCTTTCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA(G/J)TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACCTACCCGTTTTCACATACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGG
WI-19911b	116	AG ---	---	TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGCT TTTAGTCTTTTAACTGAGTTTAAAAAAAATAACAATGCAATTTT(A/G)ACACTGTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165	AG ---	---	GTCTCAAGGGGGAGAAAACCTGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGA(A/G)AAGGGAGTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156	AC ---	---	GTCTCAAGGGGGAGAAAACCTGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA(A/C)AGTTGGAAAAAAGGGAGTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47	AG ---	---	CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA(A/G)TATAACATTAGAAAA GCAAAATCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTCCACACTGGAAAATGAAGGCAGTTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	TC ---	---	GGCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGACTTACACATTCAGTTTGACAG T(C/J)GAAAAACCAACTGGAGCTGCTTTCCAAAGAAATGTTCTGTGCTTCAAAATAGGAATTCATG TTATTTCTTCTTGCCTTAAGCTCTTATCTTTCAAAATGACCTAAGCTGA
WI-18846a	49	GA ---	---	GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCTT(G/A)AAGCTGGGAGCGT GGGCTCAGCAGGCGTGTACCTCCATCCCGTAAGACCTCTCTTCCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	GA ---	---	AGCAGTGGCCTTATTCATCCCAACACGCTCTTTCAGCAGGCTGCCTCCTTGTGGCAGCAACGGC ACAGCTAATCTACTACAGTGTCTTTAAGTGAAAAATGGTCGAGAAAGAGGCACCT(G/A)GGAAAGCCG TCCTGGGCTGGCAGTCCGTGGGACGGGATGTTCTGGCTGTTGAGATCTCAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTTCTTTTGGCCTTTTGCAACC

WI-20146	31 T C ---	---	---	TGAGTCTTCTGTAATTCATTGAGCAGTTAGCT/CJCATTTGAGATAAAGTCAATGCCAAACACTAGCTCTGTATTAAATCCCATCATTACTGGTAAAGCCCTCATTTGAATGTGTGAATTCATACAGGC
WI-18922	74 G A ---	---	---	TAGGAATTGGTTTCAGCCCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTACCTGGACTTAAGC/GATCTGGCTCTAATTCACAGTCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCAGAGGAGCCACAGTTCTC
WI-18763b	53 A G ---	---	---	TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA/GJTATTTTAGAATGTACCATAATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18763a	38 A G ---	---	---	TGTGTTTTGCCAA
WI-18771b	75 G A ---	---	---	TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGA/GJTGACGATGATGTGAATATTAGAAATGTACCATAATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18771a	57 A G ---	---	---	TGTGTTTTGCCAA
WI-18820	70 T C ---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGGAACAGAA/GA/AAATAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18742b	51 C T ---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGA/GJAGATGTTGGAAACAGAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18882	94 C T ---	---	---	GGGAAAAATTTGAGACGCAATACCAATACTAGGATTTGGTCTGGTGTTGTATGAAATTTCTGAGGCC/CJT/GATTAAATCTTTTCATTGTATTGTGATTTCCTTTTAGGTATATTGCGCTAAGTGAAACTTTGTCA
WI-18970b	167 G A ---	---	---	ACAAAGTCCTGTAGCCCCCTCACCTTTCCTGTTTTCTACATTTGCCAATGTA/CJTATCGGGTTTGGTTTTCTTGATTATTTAAACGGTTGTGTTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGAGTTTTACC
WI-19970a	126 T C ---	---	---	GTGTGTCCAAAAATGGGGTCTGCTCTGCTACCTTGAOCCTTCCCTTCTCCTCTCTCTCTCATCATCATTCATTTCCCAACAACATCCTCTGCCA/CJTACACAACAAAACGTAAGTTTCATTTGGGCAAAAATTGA
				GC
				TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCCAACC
				GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGCTGCCCTTCCCTGCCAGTTCCCTCACTGCGGGGAC
				AGCAAAAGGCTTCTCACTGGGTTGGTCAAAAG/GATAGTCACCTTGGCCTGGTGATCCACAGAGGA
				TGTTGTTCAAAACCAGAAATCTTTTAAACGACTGACCCTTCCCTTAAAAACAGA
				TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCCAACC
				GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGCTGCCCTTCCCTGCCAGTTCCCTCACTGCGGGGAC
				ACCAGAAAGGCTTCTCACTGGGTTGGTCAAAAGGTAGTCACTTGGCCTGGTGATCCACAGAGGAT
				GTTGTTCAAAACCAGAAATCTTTTAAACGACTGACCCTTCCCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTAGGCTCGAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAAAT/ GACATAGTATTCTCTCTCAAGACGCTGGGGGAAATTATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTAGGCTCG/CJAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCTCTCTCAAGACGCTGGGGGAAATTATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTAGGCTC/CJGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCTCTCTCAAGACGCTGGGGGAAATTATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCC/CJCTGGCTG TGCACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTT CTCTGGGCTAGGCTCCTGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCTCTCTCAAGACGCTGGGGGAAATTATCTCATTATC
WI-19106	247 T C ---	---	TTATCCAGCCCTACCCCTGTTAGTATTTTAGGAGACAGTCTCAAGCACTAAAAGTGGCTAATTC AATTTATGGGGTATAGTGGCCAAATAGCACATCTCCACGTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGCTCTTGAGAAAGAAATAATGTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAAT/CJTG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACAATCTTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC/CJGTGTTAATTAATTAATTCACAATATAAAGTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTTCTTCTTCCCTTAATAAATTAAGTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGAGTAGGCACTCTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTCTGTAATACAACTAAATATTATGCCCTCTTCTCAGAGTCAAAAGGAAGTGGGTTGGT TTTTGTTGCTTTTTAGATTTATTGCCATGTGGGATGAGTTTTAAATGCCACAAGACATAATTTA AATAAATAAATTTGGGAAAGGTGA/CJACAGTAGCCCCCATCAT
WI-18932d	177 C T ---	---	CACACCTCATGTAGCCTCAGGAACTGGAATAAGCCTTCGAAAGAAATTGCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTGTTGCTGATTGACCTTGTATTCAAGTTAACTGTTCCC CTTGGTATTGTTTAAACCTGTACATACTTTGAGTTCA/CJCTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGTAAGAACGTCCTTGTGGAAGACAAAGTCTGTGGCTTG

WI-19042	193 A C ---	---	TTTGTGAGTGTGCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAACCTTTGTCTTCAAGGACATTTGGTGAGAGTCCACAG ACACAATTTATACTCGACAGAACTTCAGCATTGTAATTATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGATTAACTATCTTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	ATTGGCCCTGTACAGTTTGCTTATTATAAATTCATTAAAACACTACAGGTGTGAATGGTTAAAA TGTAAGCCCTCAGTTGATTTTTCAGTTATTTCTGAGTGTGCAGACAGTATTTCCGCACTGTATTAAAT GTAACCTTATTAAATGAATCAGAAGCAGTAGACAGATGTTGGTGAATACAAATATTGTGATGCATT TATCTTTA/CJATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGAAT
WI-18851	90 T A ---	---	GCTTCAATTGGCGATTGATTCAGTGCACCAATGTAACAGGGTTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCTTATTGTATCTT[A/GTAATATAGGATCCTGGAAATGAGACCTGGTGAA
WI-18821b	76 T C ---	---	TCACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/GGGGGTAGCCATTGTGCAGTCAATGCCCGGGGAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 CT ---	---	TCACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A/CJTAGAGGCTGGGGTAGCCATTGTGCAGTCAATGCCCGGGGAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	ACTCCTCTGCTGTCCAT[C/G]ACTGTCTTTTGAACACAGGAAAGTCACAGAGTTTAAAGAGAA GCAATTAACATCCTGAATCGGGAACAAAGGTTTATCTAATAAAGTGTCTCTCCATCAGCTTG CTACCTTACCCACACTTCCCTCTGATTTGCGTGAGGACGTGGCATCTTACGTACGTGGCATAAC ACATCGTGTAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---	---	TGGAAATTCCTTTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAGGGTCAAGTA TGG[C/C]TAGGGAAACATTCCATCCTTGAGTCAAAAAATCTCAATTTCCCTATCTTTGCCACCC TCATGCTGTGACT
WI-19037b	155 A G ---	---	CACGGTCTCTGCATCGTTACAGAGCGCCTTCTGGTCTAGCCAGCCCTGTATGACGGCAATA TCCCCAAAGCTTTGGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACCTGGGGGTGAAGTGTGTGACACAGTGAATGGAGGTGG
WI-19037a	47 C A ---	---	CACGGTCTCTGCATCGTTACAGAGCGCCTTCTGGTCTAGCCACG[C/A]CCTGTATGACCGCGCAA ATATCCCCAAAGCTTTGGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCCCTCCCTTACGAACACAAAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACCTGGGGGTGAAGTGTGTGACACAGTGAATGGAGGTGG
WI-19064	66 T C ---	---	TTGAGGAGGTGGGGTGAACCTGCTCCTTGGCAGGGATTTGTGACACTGCAATTCGTGGGCTGTTCCTC C/GGGGCTCTCTGGACCTTGACCCGTGGATACCAGGCCATGTGCCATGTTATTTGGGTCCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	AGCCTGTGGCTTATGTACCCACACAGAGGGTCTGAGAAGTCTGGCTGCCTGGATGCCCTGCCCTCCCTCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGAAGCAGAG/GTCTTGTCTGGCCATGGAGCC TCATTGCAAGTTGTCTTGAACACCTGAGGCCCTCTGTGGCCACCAGGCACTACGGCTTCTCTCTG AGATGTGCTTGGCTGGCTGAGCAGACAGTCAAGTGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	GTITGCAAAACCAACATGTGCTCTTTTCAGTCAATCACTGTTTTAATATGACATGGTAGAGAATAAG GTTTATGGCAGGTAAATTTTGTAAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCA/C/AJCTCAACACTATTGAC TTTGGGGCTGGATAGTCTCTGTGTGGGGTTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---	---	GTITGCAAAACCAACATGTGCTCTTTTCAGTCAATCACTGTTTTAATATGACATGGTAGAGAATAAG GTTTATGGCAGGTAAATTTTGTAAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGAC/JTGTATACAGAGGTTCACTCAACCTCAACACTATTGAC TTTGGGGCTGGATAGTCTCTGTGTGGGGTTTGTCTGTGCACTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCATTTATTTCT/CJGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGGCCCC ACCCTCATCTAGAAACAATCTCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACTCCAAGCCATG AGTATAAGATTAAAGCAGTTACTTTTGAACAAGGAAGTGCAATAAGCAACTCAGTGTGCCCC CTTAGGGTGGGAGCTCTCC/C/AJCTACCACTCCCCACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTAGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACTCCAAGC CATGAGTATAAGATTAAAGCAGTTACTTTTGAACAAGGAAGTGCAATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTCCCTACCCTACCCTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTAGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCAGCTCTGCATCCTTGTCTTGAGGGTCTGTGTACGGCCCCCTCAGGGCATGGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAGCCAGCTCTAGAGGCTCCA/GAJTCAGAA CTGGACCCCTTAACTACAAAGGAATCTTGGATGAATATTTTAGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCCTTGGCCTTGCAGCCCCATTCAAGCAGGGATGGAAGTCACAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGTGACATCTGCCCCTTATCTGTCTCTCTT CCCCAGTCTGTACACTTGGCAAGCAGAGTGTGGCAGACCCAGCCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGCGGTCA/TJGJGTGATGGCTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTTAAATGAATACTTGTGTG/JCJGATTTCAAAAAAGAGTATTAAT ATTTTGTGACTGCATCTGTAATGAAGACACTCAAAAGCCATGTTTCCAACCTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTCTGGGCATTGCTGCAATATCTCTGGCCCTCAAGTGGGAGGCCACGTG GGAACAAGGCCTCAGAAAAACAAGGACATGACGCTCCCTGAGCCAGTTCTCT

WI-19766b	93 A G ---			TGGCTCAATGACTGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAGTC/A/GJGACAAACAGAAAGGCACACCAAGCCTGAACCCCTC CGGACAACAGCAGAGTTACAGCTGAGGATGTCCCTGGAGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTACCCCTCCTCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---			TGGCTCAATGACTGTGTACATTGGAGAAGCTG/AJTGACGAGCATCCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAAAGGCACACCAAGCCTGAACCCCTC CGGACAACAGCAGAGTTACAGCTGAGGATGTCCCTGGAGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTACCCCTCCTCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---			CTTCTCTGTTGGCTTGGCAATTGTGGATTGGAAAAACCACTTGGAGAAGGGACTTTCCTGCAA AACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GJAAAGC TTAGAAAGGAACCTGAAATTGCTTCTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCAGGCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---			CTTCTCTGTTGGCTTGGCAATTGTGGATTGGAAAAACCACTTGGAGAAGGGACTTTCCTGCTG CAAAACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAACCTGAAATTGCTTCTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCAGGCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---			GGGCTTAAATTCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGAAAGGATCGCACCTTTTCC ATAACCCCTTCTACATTGGAAGAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTAAACG GACAAAGGTAAATCACAGCTAACAAACGTGATGTTGGCTCACACGTAAACCAACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---			TGTTTGAATAAAAATTTCCATGGTCTTAATTGAAGTGTATGTTACTTCTTTTGAATATCCTTTT TTCATTAAATATTT/CJ/TCTAACCACTCTATGTGTTCAACCTCTGTTTAAACACTAAGATATGGGT TTTTGGAAGGCCACAAAGTCACAGCTCCATGAAGTGGGCGAATGGTCTTGTGTTTGGAAAGCTCTC CAGGGTGTCTTCCAGAAA
WI-19909a	29 T C ---			CCAGAAATAAGCCCTGAATATCTCTTTCT/CJTTAAAAATAATTTTCTCTTTTGTCTCTTCCAA GTAAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGCGGG TTTTTCTTTTATACCTTGTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---			TTGAGAGGCTGAGAGAAGGCTGTGAGACATTGTAATAGTGTCTAGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAATGTGGAGCTGATGAGAAGCTACTGCTCCATTGTTTAGCAGGA GGCAGGAAAGTGAATCTGGGCTCTCGGAGGAAAGCGTGTGGTAATATTGGGTGACGTATGC ATCCCCCATGCATTGGTTTJG/JATGTCTCCAGTGAGCTGTGGGCAAGTCT

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WI-20113	60 T C ---	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAAAGACCTGAAATACTGTCJGGA AACAGTAAAGCAAATTACCACAAATTAGGAGGAATTTTTCAGACATAGGATATTTAAACAT CACTCAAATACTGGAGCATGATTCAGCAATAATCTATTCCATAAACCCAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107 G C ---	---	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCAGCGTGTGGC CAGTCCCAACAGGAGCAACACTTGACTTCATTAAAGGCAAAGCJCTTTACTCTGTACTTTTCCTC CCACATAGTTTAAACCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72 T C ---	---	CCTGCAATCACAAAGTGGAACTAGTTGATATTTGAAATCATACTTGATTTAACCCACCTTCAGAAA TTCTATTCJAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 A G ---	---	CTGGATTTTAATATTTCTGGCCTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTCTGTAAACATGTTTGAAGATTCCTTAAGTAAAGTATTGACGACTGAGACTAGTCGGGCAAA GTCATGAGACCCCTTAGCTGATCTCATJAGJAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 C T ---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCATGGCGGTGACJTGTCCTCTCCAGGCTCATATGGATGTCT CGAGGTGCACAGGGAAGTCTGCTGTTGTAGAAGCTTCCTC
WI-19348b	98 G A ---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCATGGCJGJAGTGACGTCTCTCCAGGCTCATATGGATGTCT CGAGGTGCACAGGGAAGTCTGCTGTTGTAGAAGCTTCCTC
WI-19635	98 A T ---	---	ATTAGTTCGTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAATAACAGTATTATJATCTTTATTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTGCTGAAAGAACTTTGCCTT T
WI-19641a	46 A G ---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGJGJTATTATAGTCTCATGTTT TTAATTTATGAATAACGTCTGATTCATTGATTTTGATTTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGATGAGGTAGTATTTAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52 C A ---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCTGGACACATTATCCCTTCJAJGGGTAAACCCAG GACTATTGCATGAGCATTCCTTAATACGTATTTGATGGACACAAGTTTTCATGTCTATTA
WI-19673b	180 C T ---	---	TCTGOCATGATCACATTGTGATGAAGAACAATGATGGTCACTAGTAGGTAACCTTCTGTGTCTATGCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGCATCACCACCTGTAATCTAATAGT GAAAAGGCAATGATGTCTCAGTATCAGTGTGAAACATTTTCJCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCACAAAAAACACAGCC

WI-19673a	35 GA ---	---	---	TCGCGCATGCACATTGTGATGAAGAACATGATG[A]TCACTAGTAGGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGAATTTACCTACCCCTGCTTTTGTCATCACCACTGTAAATCTAAT AGTGAAAGGCAATGATGTCTCAGTATCACTGTGAACATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCACACAGTCAAAAAACACAGCCC
WI-19724	35 AG ---	---	---	TTTATTTGGAAACAAAGGATTGTAATTTGGGTAA[A]GCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTCTCTT
WI-19307	196 TC ---	---	---	TCCTCTCCCCCAACTAGATGGTATTGATCACTCTGCCACAATGGTACCCCTTCAGCAAGAAGCTG CAAGCCCTTCTTGATTGCTTCATGAGAAATGGTGGCTGGGATGGAGTGACATTCCTTGCTGT GGTAACTGCAAGAAAGGAACACAGGCAATGTATCCATAGAGGCCCTTAAAGAGACCCG[T/C]TGG AAATGGGCCATGGTCTAATTTGGGTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85 AT ---	---	---	CTTTCCCTCATCCCTCTCCACACACCATCCGGAAAGTGTCCAGGATTCCTGCCCACTGGC CATTTGGAGTGTGCC[A/T]TTGGGTAGCAATGTGAAACCAACAGGCCCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTTAGGGCCCTTTGCCACTTGTCTCATAGGCGAGCTCG ATCTCTCATCTCTGGACAGGTGGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122 CT ---	---	---	CAATGGACTGAATGAGTGGTGGTGGGGTGGGCACACACACCTTCAATACACGTCAGGTCG CTTCCAGTTTAGAAAAACAGAAATCTGCATCTCAGCTGAGCGCAGCAGAGAGGTC[T/CT]CTCCTG ACCCAGACGCACTCACGAGCCAGTCCGTGTTTCAAACTGCAATTAACCTGGCCAGAGAGTTCAAC CGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141 GA ---	---	---	CACAGCATGGTGAATAAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCAATAATAATTATA ATAATATACATCAAGTAAGTTACAGCACACATTTTAGGCCAAGTTTGGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAACGCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCAAACAGAGCTTCTGAACTCTCTGGGAGGTAGCTGACAAG
WI-19076	40 GA ---	---	---	TTGGTTGGATACCTTCTGCGAAAAAAGCAGTTTAA[T/G/A]GTATTCAAAAATACCTTTTAAAAA GTATCTAGCACAAAGATTTTCTGTAAGTAACTAGATTATGTGTAAACCTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCTCTATCCAACTATCTTGGCTCCTGAAAAAAGTGCAGA AAGGCACCTGAAAGCTGTTCTTTAAGATATGGGATTTCTTTTATCTT
WI-20218	26 TC ---	---	---	CCACACACTCTGGTTTATAAGCTA[T/C]JAGGACAGAGCAGAGATGGAAC TGAAAAACAGGTTAG AAAATAACATAAATTGGAGGGGAACAGTGGGATGAGAAAGAAATGACAACAGCCACATGTGCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAGATGCCAACCAAGTCTATCTACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154 TC ---	---	---	CAACCTTTTGCAGAGGGGAGCTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAAATCCTCTTTTAAATATCTCCAGGCTTGAATGGGAGGGGCTGGCTCTACCCCTTCTCTTCCA TCCAGTCTATTGCCAGAT[G/C]CAGAGAAAGCGGGGAGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGGCTTCACTCTGTGCACTCTCTCATGCTGGGACTTGTCTTTCCGGG

WI-20361a	192	A	---	---	CTGGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGGCTTATGCAAGATGACAGAAATATGTGAAATCTGATTGTCCAGAGTTACACTCTGCACTCCCAAAGCTACAACAGTGCCACAGCTGAGAGGTTTCCCTATACTTCTCTACTACTGTGACAAATTTAGCG/AJATCCTTC
WI-20572	75	A	G	---	AAATGGGAAAATTCCTAACTACACGAGACAATGGGTCTACAGTAGGCCCGG GAGCCAAACCCAAACAAACAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTCTTCTCTCAGAAATTG/JTCATAAAACATCATCTTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTTCA AATTCATCTTTCTCAAAATTTTAAATTTGTTTTAATCCAAAGGTGCTTATGAATTCCTCAAAAATA AACTGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTGATTAT CATGACAAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATAGTATACAGCAATCTT TTCACATTTTAAAGAAAATGTGAGATCCTTTGTGGTTTTTATTTCCTTAAGTACAAAATGCTAAAAC G/AJGGAGCCGAGCTCTTCCGCATTACGG
WI-20588	133	A	---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTCAGTCTGTTGCTGTACTTCAG/AJTTTTTAAATCTGGGAATGAGCATGACGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAGGAACCTCAGGATGTTGTAGGAAGGGGAGTGATGCCAGGCTTCACACAGACTAT CCAGAAGCCATTCCATGGGGTATTTGGTCTGCATACCTGTGAGACACTGAGCT
WI-20593	79	A	G	---	TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTGCTCTCATG/JATGTATCT TGTCCTGCTGTCTTTTAGGTTAGCAAGGTGTATGAATACTTTTAAAGTTTTGTTGTTCTTTTCCCTCGT GGTATCAGTGAATACTGATCTATTCTGTGGTAGGGTCAATTTACAAAATGGCCATGGAACCTGAGC AAAAGCCACGTGGGATAAAATCACTCACTCACCATCGACGCCACCAGTATT
WI-19765	57	T	C	---	TGACAAAGGAGAGAAGGGAATTCCTACTCATTCGAAGGAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTGCTTAGCCAGTCCAACTCTACGAGGAACCTGG CATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTACAGT ACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCAGT/AJG/GTTTTCTTTTA
WI-19066f	239	A	G	---	TGACAAAGGAGAGAAGGGAATTCCTACTCATTCGAAGGAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTGCTTAGCCAGTCCAACTCTACGAGGAACCTGG CATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCTCCATATTC/JJGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTATTCTTTT
WI-19066g	184	C	T	---	TGACAAAGGAGAGAAGGGAATTCCTACTCATTCGAAGGAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTGCTTAGCCAGTCCAACTCTACGAGGAACCTGG CATATGTTCTTGCGT/JJGGTCACCCCTGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTATTCTTTT
WI-19066f	148	T	C	---	TGACAAAGGAGAGAAGGGAATTCCTACTCATTCGAAGGAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTGCTTAGCCAGTCCAACTCTACGAGGAACCTGG CATATGTTCTTGCGT/JJGGTCACCCCTGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTATTCTTTT

WI-19066e	147 GC ---	---	TGCAAGGGAGAGAGGGAAATCTACTATTGCAAGGAAATCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTCTAGCCAGTCCAAATCTCTACGAGAACTGG CATATGTTCTGC/GC/JTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA
WI-19066c	100 GA ---	---	TGCAAGGGAGAGAGGGAAATCTACTATTGCAAGGAAATCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATC/GAJTCTTAGCCAGTCCAAATCTCTACGAGAAC TGGCATATGTTCTTGGTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA
WI-19066b	87 CT ---	---	TGCAAGGGAGAGAGGGAAATCTACTATTGCAAGGAAATCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTCTTAGCCAGTCCAAATCTCTACGAGAAC TGGCATATGTTCTTGGTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA
WI-19066a	72 CT ---	---	TGCAAGGGAGAGAGGGAAATCTACTATTGCAAGGAAATCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATGCTCTTAGCCAGTCCAAATCTCTACGAGAAC TGGCATATGTTCTTGGTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA
WI-20860	105 GC ---	---	TTTACAGCGAGTTTTCGGTCTCAATAAGTATGAATCAATAGATTAGGGTGAAGAAATGTG TGCTAAATAAATCTCCCTTTTGAATGTATATTGT/GC/JTTAATAAGGAAAGCATTAAATTA CAGACATATTTACAAGTTCTGAACATGAGTATTCCTACTGTTTCTGTACAAGATAGAACA AAGCTATCCACCCGCCCAAAATACTGTTTAAACAACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCTCCCTCAGCTTCC TCCACCCGCTCTTCTTCCAGCCTGCTGCATGCTGCACCCCTGGTCTGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120 CT ---	---	TTCCCAAGGGTCTGTATTGGAGTAAGCTCAAATG/JATTTAACTTCTAGTTGCTTGTCTTTC GTCTTCTTCCAATGATGCTTACTACAGAAAGCAATCAGACACAATTAGAGAGCCCTTTTCCATAAA GTGTAAATTTAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-19087	37 AG ---	---	GAAAGCCAGAGATTAGCCCGCATTCGGCATCTGTCAACCAGGACAGAA/JTGCATGGACAAGGGA TGAGCTTTACAAGATGATGCACCTTTGGAGATCAGAAAATTCATATTTAAGCAAAAGTGATACAAACA CAGTGATTGGGAATGCCT
WI-18790	49 AT ---	---	AGGAGGCTGTTCCAGGATCCTGCCAGCAGCCTC/GAJGTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCGTGGATCCTGCTCTAGGCTGGACAGAGGATTCAGAAAGACACCAGGCTGCACA GAAAGCCAGATGGAOCTGAGTGTGGTGCACAGCCCTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA
WI-18987	35 GA ---	---	

WI-18919	26	C T	---				TGGATGAAACACAGGGATTCCGGA[CT]GCCAGACCCCATTTTATCTTCACTTTTCTCTACAGTG TTGTTTGTGTTGTTGTTTATTTTATCTTGGCCATACCACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64	G A	---				CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCAATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	G C	---				CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCAATCAGTCAATCA[G/C]ACAGAGTATCTCTGCTCTAGACCTGG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	T G	---				CTTCTGGTCAAGGCTTTGGACAT[G/C]CTCTCAGTCAATCAGACAGAGTATCTCTGCTCTAGACCTGG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	G A	---				TCAGAAAGCAGACATGGCATCTGTTCCCTTGGTCTGTTGGTTGTGTACCTTTTCACGAGACCTGAATT TTAGAAATGCCAGTGGTGGCAGAGTGAGTGAGTAAATCTCCTTTACAGGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTATCAACATATCAACCA[G/A]TAGCATTAAACCCATTTTATTCCTGTCCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAAGGCAGCATGCT
WI-19212	46	T A	---				CCAAGTTGCATCCATGTTTGAATTTCTGATGAGACTAGAGTGACAGT[A/G]TTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCCTATGGAAATGCAGCTGC ATAATTAAACACATTATCAAAAGTCTCTTACAATTTATTTCCGCAGCATGTGAGCTAAGTAGACOCA ATGGGAGAGAAATGCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210	G C	---				CTGTGAAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAGCACACATTGGATG GCAGCATGGGTTTCTCCCATTTTATGGCATGAAATATGTGGTTTAGAATAAGGAACAAGCATTATT CCTTTGCCAACAGCCTCACTCTAAGAGGCTTTTGTGAGTCAAGCAACACTTGGCTGCTCTGCC CTTGGAG[G/C]TGCAATTGACCTGCTCTCACTGGTAAAGGTGACTTGGTGGC
WI-20014b	214	T C	---				TTGAAATCCAGTCTCTGCGCCGCCAGGCGGTCTGTACCATAGATGTCTTCTCTACTGGGGTC GTCTGGCTTTTGTAGAAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTACAGAGCAATGTTCTTGTATTCTGAAACTGGAACTGAACCAAGTTTGCCTTTCTCTAGTCACC AAGCATACTT[C/T]CTCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198	T C	---				GTCTCCCCAGAGTCTCTGCACCCCGCCCTGTCTGCTGTAAAGGGATACAGAGAAGCTCCCGG TCTCTGCATCCCTTCCAGGGGGTGGCTTAGTTTGGACATGCTGGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCAAGCTCATCACACAGGGGGCCATCCTTCTCAATACAGCC[C/G] CCCTTGACGTCCCTATTTCAAAATAAAATTAGTGTGCTTGGCTGTCTGT
WI-19135	20	G A	---				CAGTTACCCTGCTTTGGCTC[G/A]AAAGTGTCAATTTGTAATTTTAGTATTAACTCTGTAAAAGT GTCTGTAGGTACGTTTATATTATATAGGACAGACCAAAATCAACCTATCAAGCTTCAAAAACCT TTGGGAAAGGGTGGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAACCTGATTTTATTAACT GCTTTGGCCATATAAATGCTGATATTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54	G A ---	---	---	TACACAGAGGGTGCACCTGGACTCTGAGGGTTGGGTGTGGAAGGGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTCTGTGACCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACCTTACCCTTTTTCATAGGGGAAGAGTGTACACTCTCTGGCTATCTCAGGGGAATGGGAAAAAG AATCTTTCAAGGGCAAGAACTCTGTGGAGGATGTCTGTGTATGTATACT
WI-19144	222	G C ---	---	---	GTGCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTACGCCCTTGTGACCTCCCAGCCTTTCTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGTGAGCTATCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGGCTGTAGCCAGGAACCCCTCTCTTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110	C A ---	---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGCTGATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACACTAG[C/A]ATTTACGGGTGTGGGCAC ATGGGTGTGGCACCCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGCTGATTTACACGAGGGTAGA CTGGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACCCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACTAAACATGAAGGAAAGGGTGCCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTGCTGTCGCTGTCGCTATGGCAGAGCATT CAGTGCCACCGTTTAGG
WI-19235	173	A G ---	---	---	TTCAGGAGGTGGAGTTGCTGTCAGCTCTCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCCTCTTCACTGCCCAAGTATTGCTGTGATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTTTCACAATGGTGGAA[G]GCTTCATGTAATATGATCAGGACCCAC TCCAGTCTCTTGAAAGTGTGACAGTGTCCAGCGGTTCTGCAGCACTA
WI-19222	179	C T ---	---	---	CGTTTCCCTAACTCACCAGTTTGTGTTGGATGATTGATTTCTGTGTGTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCCTAAAGGGACTCTGCGGAAC[G/T]TTTACACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTGTACACTGACGTGTCCAGAGCAGCATT
WI-19117	134	A G ---	---	---	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCACTAAGACAAGAACATTCTCTCATAGAACATTG ATCTGTTTTACAGGAAACAAACCTTGCCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A[G/T]AGCTATTTTTTCCCTAAGACATTTTTCATTTCATGAATATTTCAAGTTTTTCATACTGTACA CATTCTTAAACACATGATACCAGCAGCACTGAAATGAATGCCGAATTTG

WI-19134c	263 C T ---	---	CTCTGTTCGTGACCTGACAGGGTGACACAGCCCTTTTCACACTCTGTCTCTCTATCTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCATCCAGAGGGGTGCAGCCAGGGTGCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCATCTCTTTTCAGAGCAC TTATCCACTTGTCTCTCTCTACCTCGGCACCTGGGTGGAAAGGG
WI-19134a	162 T C ---	---	CTCTGTTCGTGACCTGACAGGGTGACACAGCCCTTTTCACACTCTGTCTCTCTATCTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCATCCAGAGGGGTGCAGCCAGGGTGCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCATCTCTTTTCAGAG CACTTCATCCACTTGTCTCTCTCTACCTCGGCACCTGGGTGGAA
WI-19224	112 C T ---	---	GGTTTCACAGTCTTTCCAGGGAACTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCTCTCAGGATGCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTTTCATAATCCAGCGCCAGAAAGACTTCG AGGAAACTCATTCAGGAGGTGAAATGATGGATGACTCTCCCAAGATGAAAA
WI-19201	179 T C ---	---	GCAGCTCTAAGGACCACCTGGCCATTAGCTCTGGTTTGTATGGCATCTCTTCCACCTGTCTCTC CTTGTCTCTCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGAACACAGCCTCACACTGCC CTCCGCCCCACACTTTGCCCTGCAGGTGCACCGAAAGGACTCTGGGGGATAAAATTCAAAAA GTGTATGTCTCTCAGAGGTGACACTCCATGTCTGGCTTGGCTCAA
WI-19034	45 T C ---	---	GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGAAATCTCCTCTATTACATTAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGTCTGTGTTGAAAGTGCAATATAAATTTTGG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTTCAGCATTTAAGTCTGTGCAATTGAC ATTGTCTACTTAAACTTAGTCCCTAAGTCTCTTATGCTGTGCTATATA
WI-19102	25 C G ---	---	TGTTCTGAGTCACGCTGAGGAGAGCTCTTCTCACTCAGGAGTTCATGCTGAGATGATCATGATTCA TGCGACGTATATTTCTTTGGAAACAGATGAAGCAGAGGAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTGAAAGCTAGAACTCCTGTAGTTTTGAACCTCAAGGGGAGAAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGCATCATCTCCAGTCCCTCACTGGGGAA[A/ G]AAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ---	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGCATCATCTCCAGTCCCTCACTGGGG[G/A] AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---	---	GGCAGCAGCTTTTAAATTTGAACACTTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTTCJAAGATCCACAATTGCAAGGCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121 C T ---	---	CAGAGGGAAAGTTTATTGAGTCACCCACAGAGGAACAGAGAAACAGACACAGGAGTTCTGTGT GCATGGAGGAAATCAGGGGCGGNACAGCTGAACCTGCGCAGGACAGAGGGGGCGCTGGACAGCA GCGCATGCCACAACATTCA

WI-18017	87 C A ---			ACAAAGAAATGGAATAGGTTGGGAAACCTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATTAATAATTATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101 A G ---			TTATTGCGTTCCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTCAGAAACNCGATTCTGAATATCCC[A/G]TGGCGCATATGCAAGGAGATGA
WI-18254	64 T C ---			TATACGGATCATGTATTTGTGTGACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCAC[T/C]]GCCAAATCCCTCTTGGTTCCTTTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18265b	117 C A ---			CAATGGGTGGACTGAGTATAAACGCATATTGAGAACAAAGACGGCCTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTTGGGTGTTTCTCAG
WI-18295	40 C T ---			ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TGGGAAGTAAAGTTGATTACT TCCTCTCCAAGGATGATATGTTTAATGAATCCCTTTCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64 T C ---			GGCAAGAGACAGAGATTTAATTGAATAAAACCTCCAGGCTGTACACGGTGGGAGACACAAA[T/ C]GAGTAATTAACAACATAATTTTANATGACAGTGCAATTAATTAAGTCTCTGGTAAAGCCAGAG GGGAGGAGGGGCTTTCA
WI-22585	56 A G ---			TTTATTTAAATTTGCATCTGAGATAATAAATTTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGCGAGTATCTTCATTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G ---			GGGCTGTGGAGTAACAGAACTTGATGGAAATTGGC[A/G]TCTGTGTAGATGATCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---			GCCTTTGCTCTTTGCTGCTCAGAGCCTCAGATGGATACGCAGCACTCTCTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAG[A/G]GATCCAGCAGTGAGATCAGGCAGGTTCTGTGTGCACAGACAG GGAACAGGC
WI-19888a	98 C T ---			GGCAGGATTCACCCATAACAGAGAAATAACTCCTTATTGGAACAAGGTTTATTTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTG[A/C]TGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCAATTTAAATGGTAATTTTCATGTTATGTGTATTTACCTCAATTAAGAATGGAACATGT CTTATAATTGTAAATTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T ---			TGAGACCATCCTCCTCAACAAAGATCAGTCAGTTCAGCACCTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]TTGTGCACACAGTACAGTGACAAATCCAGAGGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125 T C ---			TCAGAAATGCTTCCACTGCCCCAACCAAAAGAAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAAGTTAAAGAAAGGTACCTCTCCTGGAGTTGCATGACAGGATTAGTCTCTCTGTTT[C]CTGGT GCAAGTTTGAACCAAGTATTATGTACCAATTGCAATGATCAGAGCATCTGTTCCCTGTCAGATCCCCACTAG

WI- 20561b	94 T C ---	---	CGTTGCTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATGTC/CJGGAAATCAATGTCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---	---	CGTTGCTTATTAAAGATGGCTGTTT(A/G)JAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATT TTGACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---	---	GCTTTCATTTTCTGTCACCCACCCCTGTCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT AT/AJATAAATCTATATCATATATTATACACACAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGCTCTCCCATGCCACTTAAAAATGNCACAGGTTTGTCTCTATGCAA GAATTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ---	---	GCTTTCATTTTCTGTCACCCAC/CJGCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTATAGAA CATATAAATCTATATCATATATTATACACACAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGCTCTCCCATGCCACTTAAAAATGNCACAGGTTTGTCTCTATGCAA GAATTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ---	---	GCTTTCATTTTCTGTCACCCAC/CJGCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATAAATCTATATCATATATTATACACACAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGCTCTCCCATGCCACTTAAAAATGNCACAGGTTTGTCTCTATGCAA GAATTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ---	---	AAAGATTTGCAGTCTGGGACACAGTTTGGAAACACTATTTATAAGTTGCACATATTACAAACAG NTCCAAATGGTGAACCTGGTATTCTAAGATGAAGCTTAATGAACATAATGAAGTGAATAAACGGC G/AJGTGAACATAATGTTAAAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTTATCCCTTTTCAGGTTTCGATT
WI-21444	39 A G ---	---	CTGGGAGCAAGTAACCATTTTAAAGAAATACTCTCAAC/AJGAGTTCTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATACTTATTGGAACATAATCTTTGTATTTATTCGAGGAAGAAGATCT ATAAGATTGACTTACTCATTTGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI- 21034b	148 T C ---	---	AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGATGAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAAATTAAGTGGTATGG GAGATTGGATAGAT/CJGCTAACCTATCTCAATTTTAAGTAATGAGCAA
WI- 22091c	205 G A ---	---	GGCGTGTATTTGATGCAATGTCCACCAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGACAGCAATGTCATGTACATACAAGCATATTACCTCCCCCTTAAGTGACTCATAATTTTC ATTACTGTGTGTAGCTTTTAAAGGTTTAAAAATGTAGGCTTAAGTGGTATTACTTGAGGGCA ACA/GJAATACGGCTTAACACACACTAAATCATGAGGCTCAGGGATTG

WI-21805a	45 A T ---	---	CAACTGCTGAGGCTTTCACTAGCTGATTTATATACTCTATATT/TAJAAAAAATCTATAGTCTG CAGTCTTTGACATACTTCTCAAGGTGGATATGTGGTGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGCCTTTTGTAGCTTAACGTCTTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTTCATAAAATTCGAACAGTTGAAGCTGTTTTTGTAAATTGCTG
WI-21778b	155 T C ---	---	AAAAATCCATAATTATTGAACCCAGTTACAGAGAAAGTTCTGAACCTTTTATTGAATTATTGAC TCTGCCGGGTGCTGTTCTGGCTTTCAACTCCAGTCTGTCATGCCCCCTGTGTAGTGGGGTCCCCAG GTCTGGGCTTCTGAGGCTCTTCTGGTAGAAGGAGGGCAGGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGGTCAGATGGGGCAGTTGGCTCAGCTGAGTCCCTGACTCCGGAAACACTGTGCCCTCT CAATGATCTAGAGCTCATCTTGGCGGTACATGAGGGGCAAGTTGTTCTAGTACCCATTTAGCCC ATGGCTCTCAAGCCAATTCACACTGGGAAAAACACACCCTCACAAGATGCCATATCCATTTGAGTTT ATACAGGTTTTAGTAGTAGAACTAAAAACATTTTAA/CJAATTATCTA
WI-21449b	222 C T ---	---	AACAGCAGCAGTCACCTCCAAAATGCAAAAAAATTAACAATTTTAGAATAAAATTAATGTTTA TAATGCGGGTCAGAAAGANTGAAGGTACAACAGAAATCAATCACGCAGCACTGGAGGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAGCTGACAAGAGTCCAACTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCAC/CTTGACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ---	---	GCTTACAAGGAAGCCTGTGGACAGCGAGNTGGGTGGAAACCGACTCCAGCCTGGAAACCTGCCCTC CCATCCCTTGTAGGCTTCTTGGCTTCCGGCTGATTTCTTCACAGAGTCTGGCCAGGGCAAGG AGCTGTGTGGGGGGCAGTATG/AGCCAGGGACTCCCTTCCACAGATGAGGCTAGGGCTGCAA AAGGGCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178 G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCGGTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAACCAACCAACCAACCAACCAACCAACCAAG ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/G/AAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTCTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCGGTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAACCAACCAACCAACCAACCAACCAACCAAG AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTCTACCCCAAAAGTGTGGAGGAAAG
WI-21809b	146 G A ---	---	TCATGAATATGCAGCTCCATAATCTCTCCCTTGTAAACCGTCAGTCCGTTCAAGCTGTAAA AACAGCCCAACCCCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAGAAGGGAGCCTGTAAAG GATGTTTCAAAG/G/AGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAA[C/T]GTGCAGTCGGTTTCAAGCTGT AAAAAGCCCAACCCAGACATCACAGAGGCAAGAGCAGTGCGAGTGAGAGGGAGCCTGT AAGGATGTTTCAAAGGAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	ACATTCCGAGCCAGTTTTTCCATATTGCTCCACTGGCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGTGCTCTTGTGATCTGTG/JACCTCACCCATGCTGCCACCTNAGTTCC CACATTTCCCCACGCTAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCTCCCTTTAAGGGCTCA CAACTAAAGATTTACATGAAGGTCGTGATTGATTGAGCAATCTAGGGGAC/JTATGTGACAG TTTC/JGJTGCACTGGTACAGAACAACAGGGAGTTTCAAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCTCCCTTTAAGGGCTCA CAACTAAAGATTTACATGAAGGTCGTGATTGATTGAGCAATCTAGGGGAC/JTATGTGACAG GGGTTTCATGCACTGGTACAGAACAACAGGGAGTTTCAAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCTGTTTACAGGGGGGAAAAATCCTAGGNAATACTTATGTGACTTCTTG/JGJTTTCA TCATACAAGACAAGCACAAAAAGCACCACCCATGCCCTCTGAGGAACATTGGACCATGCACCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCTGTTTACAGGGGGGAAAAATCCTAGG/JAATAACTTATGTGACTTCTTGATTTC TCATACAAGACAAGCACAAAAAGCACCACCCATGCCCTCTGAGGAACATTGGACCATGCACCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACCTAAGGCCAAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAAGGA GCACAGGTAGTCCACAGATA[G/A]GACACAGAACCTCAAGCTGTGAGGTCATTTGTAAATTA AAGAATACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAGGAAC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACCTAAGGGCCGTGAAGGCATGATTGGTTTGGCACACAGAGTGGATAACCAT/JACAT TGGCTGGAATGAGGTGTCAGGAAAAATAANTGCACAAATCTAACACCATGTTGAAATCATGCTGA GTTCTGGAGAAAGTTAAAGTGTAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCCCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGGGCTGGCTTCCCTCTCCTGACAC CAGCAAGGGGAGGCACCATCACCGGCCCTGCCCATCATCATCCATGATGATTACTAGACTAGGAA GCCAACGGAANAGGACCCCGCGCTTGC/JGJTGTTTAAATCCAGGTTAAGCTATACACGTTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAAGTCCCTGTGATGGGAATGAC

WI-21681	117 GC ---			GCTTAGTCTCCACCCCTTTTAAATGTACTCTAGGTACAAATAAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATAG/CJTTTTAGTCACAGTC ACACAAAACCTACCTTCTAAGGAAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAG GA
WI-21980a	25 TC ---			TCAGTTTAAACACATTTCATCAAGGA/CJAGATTAAATATGTCAAGGTAGCATAAAAGGGAGATTAA TAAACAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTATTATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 AG ---			TGCTTGATTAAATGTGGTGTACATTATCTATTTCACAGATGGAAACAGAAAAATACCAGCTTTTTT AAA/AGTAGCAATATCTATTATATAATAAATATTGAAATAACACCATAATAATATCACTAAGGA AGTAATCTAATTGTGTGATTTTCAGAGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGTGTGTAAGAACTAGGAAGGACAGGGATTTC
WI-22457a	112 GA ---			TTGCTATAATTTCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAAATCACTCATTAGA CAACAGTAACATACCTGGACACGGTTTCAGGCATGAAGGATACA/CA/CAGTTAATTAACTAAAG GAACAGAGTCCCTGCATTCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAACTCTGGGGCC AAAACCCACTGAACCTACCCAGCTGAAAACACTGAAGGATAGGTAAGGA
WI-21524b	97 CT ---			GCGTGAGGGTTAGCGTATAATGAAAGGGTGAATAGCCTGATGACGACCTTCGCGTCATACTTAT AATGGTTAATAACAGCATTCCTGTCTACCC/C/CTGATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35 AC ---			GCGTGAGGGTTAGCGTATAATGAAAGGGTGAAT/CJGCGTGAATGACGACCTTCGCGTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 GT ---			TTACCTTCCAAACACAGGCCACTTTGGAGAAAG/GTJAAGAGAATGCTATTATCAATAAGCCAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGCACTACCATACCATCATCTCTGCCACAGAACC TTTGACATGCTGCCCTCCCTACTCCGCACTACCTGCTAATTGGGACCTGAAGCTTCAGCATCCCTT CTTAGGG
WI-21703d	197 AG ---			CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGGCGGCTC TGATCCCTTTCTCAGCACAGACCATCTTCAACCTCTCGGAAAGCAGCATTTGGAGCCTACACCA CTTGCTTTTCTCACCAGGGTAAGAAATGCAGGTTATTTGCAGAGGGGAGTGAGTCTGGGA/AG/GJ TGGGAGAGCAGCATAGGGGCAAGGACTTAAGGGAACCTTGTGGGGAAGAG

WI- 21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGCGCAGGGCTC TGCATCCCTTTCTCAGCACAGCACCATTCTTACCCTCTCCTGGAAAGCAGCATTGGAGCCTACACQ A/GCTTGTGCTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG TGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG
WI- 22663c	139 G A ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGGAGGTGAGCCGGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTACAG GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAAATCCGTGTGAATGTGGGT
WI- 22663b	55 C T ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGGAGGTGAGCCGGCTCGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAAATCCGTGTGAATGTGGGT
WI- 22663a	38 C T ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGGAGGTGAGCCGGCTCGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAAATCCGTGTGAATGTGGGT
WI-22668	99 A G ---	---	TCCTTTATCTGCTGCCTGCCTGAGTATCTGGGAATCTACAAGGATTTGAGGGAGCCCTTGGGATT CCAACCTAACAAATTAGTTTCTGTAAATATTA/GJTCTAGTCCATTAGATTGTGTAATGATCTAA ATGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAAACCTTTTATT
WI- 22631a	52 T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAATCTCGCTTCAGTCTGA/T/CJAGCACCATT CAAGTTTAGGCAAGTATTTAACCTCTCAGGCTCATTTCTCTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTTGGACAATCAACTGAAATTTTT
WI-20258	157 G T ---	---	AATCCACACTTTACGGAGGGGACCAGCCTGCCATGTGTCCTCCAGGCTCACAGAGGGGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGAGATGGTGACGGCGATTGGAACCGTAAGGCATGACAACG GGAGCCCGGGGGTGTTCAG/GTJCGGTTGACGCAAGGTGCAATGGCTGGCAGGGGGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCGGGGGAAGTACC
WI-22714	212 C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTACATTTGTAGAGAAAATCTAGGTCT ACTAAATAATCTAGTACTGTTTCCACTCTCCTGCTAAGTCTGACAGGAGTGTGTTGGGAAACGAAGT CTGAAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/C/ATGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI- 22734a	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGGCC/TG/JTCTTAGAAGACATTACCCA AATGATGAGAGGCAGCCAGTCGTGGAAGCCATAGTTTGGATGGGAGACTTTTCCGGCAGAGGAAAT AGCAAGTGCAAAGGGCCTGAGGGAGAAATGAACCTTGGGCTTGTCTACAGGGTGAAGGGCGCCGGT NTGGCTGAGGTTAGTGGATG

WI-22724	117	A G ---				TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAGTGTTTGAAGATATAGGA CAAATCAAGATTGTCAAATGTATAGTAACGTTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTTGGGAATT
WI-22750	48	G A ---				TGTAACCTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTTCTGACCATTCTGACTGTGCT
WI-22775a	60	A G ---				TGCTGTTCTTTAGTTTCATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAGGGGAAATAAACTCCCTAAGGGCAGCAATAATTCTGTCTTTGATCCTTCATTTCAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTGGGATGAGGTATGAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22808	143	C T ---				CTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACCTGATTAGAGAGTAGGTATAAGAAACAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---				TCCTCGTGTCTGAGCCCTCATCCCCACCCCTCCAAAGCCCTCATGCCACACACCCGTGTCACACATT CCCCATCCTCCCTGTCTGCTCCCATCTCAAGTCCATTCOAAGGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAGGAGGGGAGTGGAGATGGCAGAGATGGGGTGGAGCCAGTGCGCTGTGGGTC CT[G/A]TTGGCGTGTGATGTGGGGGCCAATCCTGAGGCCAGAGTTCA
WI-21031	31	C T ---				TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCATTTGCTCCAAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122	A T ---				CCATATCCAGTCTTCTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCAATTGATTTTTTATTGTTCTTCCATTTCTCTGTCAAACCTTTTC[A/T]TTTTGTTTATAA ACTGTTTCTAAACTCAGTTAATCTCTATCTGTATTTCCTGAGTTCCCTGAACTTCTTTAGAGG
WI-21186	95	G A ---				AGCGAGCATCAGAAATCACCCTAGAGGGTTGACTAAACAGACTTCTGGACCCAAACCCAGAGCTTCT GATTCAGTAGGCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCTCTAAGTGTTCAG ATGCTGCTTGTCGCCGGGAACACACTTTGAGAACTATTGTTCTAAAATGTTCTCTCTCTTTTAAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94	A G ---				CCACGATAACTATAAAGCAGAAATAGCTTTGAAAATCAATAACATATTTAGTAACACACATT CAATTTTATAACACACATAAAGACACC[A/G]GNTCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTGTCATCACCTAGGGGAATGCTAAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---	---	TTTCCCCACATACCAATGCACCTGTTTGTATAAACTATTC/GTGGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATCCCATTAATTATAACAAATAATTATTAATAATCTGTACTATTACTGCG TTAGTTATCTAGTGTATTGAGAAAGGAGAGATCAGCATAGTTTATTTCCATGTAATAAAAGCTT AACACA
WI-19937d	186 G A ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTATGACATTGGTGTCTCCTCAGCAAGTC/GA/TCCAAACCTTC CAAAAGAAAGCAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 C T ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTATGACATTGGTGTCTCCTCAGCAAGTC/GT/GTCCAAACCTTC CAAAAGAAAGCAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227 C T ---	---	GAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCAGTGAATACTGTTCAAGTTTCACAGGCTC TCTCAGAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAATACATTTCTGGGG TCCAATCACATACTTCAGGTTACAGCTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTACAGT CCTCTCATTTCTACAGTCTGATTTTC/TCTACTGAATCTTGGGTTGGAG
WI-21122a	42 C T ---	---	TCACITTTGATCATAATCCCTGTAAAGCTAAAGTTATTCA/C/TJTTAACAGGAACTCTGTTTTTCC TTATTCAAATGTACAGCCTGACCGTTACTGTACATATTTGTAGCAGGAGACAACACTGGAAATACT AAACAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCTCT TTGTAGGTTTCACAGAGCCTATTGTTGGGTTGCT
WI-21254	53 A G ---	---	CAGTTTGGTACAGGAAGGGCCCATGAATGTGGGCGGAACCTATTCACAGGAG/G/G/CAAGGAGAAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	AAGGAACTGCGATGGGTACAAAT/G/TJCCAAATTCATACTTAAGAAGGTGGGAAACGGGTCATTCT TGGCCTGCTCCAGAACAGGGGCGAGTCTATGCACTCTG
WI-21059b	181 T C ---	---	GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCAATTTCTCTATTC/TJATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGTCAAGCAGAGTATGGGTGACTATCCTTGCCTAAT
WI-21059a	63 C T ---	---	GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG/C/TJ GAACTACAGTCCAGCATTTCTGGGCTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCACTGAAGTCAATTTCTCTATTTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGTCAAGCAGAGTATGGGTGACTATCCTTGCCTAAT

WI-21627b	153 A G ---				GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA/GJTCCAAAGTCATCTAATAATTAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106 A G ---				GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC/GJTATGGATATTTATGCTAGGAATGA CAACAGTAAGGCATTGCAAAATCCAAAGTCATCTAATAATTAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21399a	75 C T ---				GGATTGAGTCCCACTTGATCTCAAATTCACCTTCTTGATGTAACAAGCTCATCCCTCTAAAGTT TCAGTTT/CJTTCACCAGTAAGGAAAGGTTTGACACAGACATGTTGGCCGTAATGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTTGTGTGTCCTAGGACTAGGTAGGATCTCTCTGCTTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTTGT
WI-20329a	68 G A ---				CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGAGTGGGTCACAGAGACAAGACATCAAT C/GAJTCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAATCCCATCTATGAGAC AGCAGTGTGGCTTCTTAAAAACAGTAAACCAATCAAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCAGAGCCCTTGAAGGAAAGGCCCTCACT
WI-21249	155 T C ---				TTCTGGCATTCAAATGTACATGTAATCCAAATTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACTTTTAAAGAACATTATAAAGGTAATT AAACTCTAGGTGTATACTTAT/CJATGGAAC TAGTTTATTTCCNATTTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTATAAACATTGAGA
WI-21504	147 C T ---				TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGCCATTAGAAAAAATAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGACAATTACAGTGGGGGACGGCCGTTCCGCTCCAGCTGGGTTTCCCC AGATGCAACAAT/CJTGGGTTCTGGCTTCTCCACTGTGGGGATGGGGATCGGCCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---				CTGCACAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAACGCGGGCAGGGAGGGGCGAGAGAC/GJACACTAGCTTGGGGGTG GGCAOCCAGCTTCAGACCCCTT
WI-21475c	181 A G ---				TAGCCCTTCTGCCAATCTGGCAATNTGAGGCTGGGGTGGAGCTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTACTTGTCTTAAAGCACAG CAGTCTGAAGCTTGGACCTGGGACGTGGGCTCTTGGAGAGGGCA/GJAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCGGTCTCCACCTATTTCCTGCCCTGAAG

WI-21475b	117 A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGAGGTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTC/A/TCTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGGCTCTTTGGAGAAGGCAAAAAGCCACAGCAGCAAC ACTTAGAGCAAGACCCCTCCCGTTCTCCACCCCTATTTCCTCCCTGAAG
WI-20893d	207 A G ---	---	TGTTTGTGTTCCAGCCACATCTTCTCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTAAAGTGTCTACTGAGGAATACAATCATTTGTCACGTAAGTTTCATCACCACCTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTCTCTCTCTTTTACAATGCAGT TTC/A/GACATAACATTGGTAGAGTAACAACAACCAACCAAGCCTAAATG
WI-20893c	179 T C ---	---	TGTTTGTGTTCCAGCCACATCTTCTCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTAAAGTGTCTACTGAGGAATACAATCATTTGTCACGTAAGTTTCATCACCACCTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTCTCTCTCTTTTACAATGC AGTTTCAACATAACAATTGGTAGAGTAACAACAACCAACCAAGCCTAAATG
WI-19941c	71 C G ---	---	GAGCTCAAGGGAAGACCCCTTACCAGATAGGACTAAGTGGAGGGTGGAGGAACCAAGGTGA GGTATC/G/GGTCTGTGTGAGACAAAGCAGGGGGGCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCAGCAGCAGGGTGCAGGAAGGAGATGGGGACATTTCTTATTCAGTGCATGTCCCTTAAAT AAACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGACAAAGCGG
WI-21552b	166 C A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATATGAGATATTTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAATGCGATCTCTTCCCTCAAGCATTTATCCATAGTTTACAAAGAA TCCAAGTATACCTTCTGATTATTTAAATGTACAATAAATTATTTGAATTTAGTTACCCCA ATTGCTATCAATAATTCAATCTTATTCATTCTTTGTAACATAATTTTGTGTA
WI-21552a	66 G A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATATGAGATATTTTGATACAGATACACAATGTG /A/TAATAATTACTTCAGAGTAATGCGATCTCTTCCCTCAAGCATTTATCCATAGTTTACAAAG AATCCAAGTATACCTTCTGATTATTTAAATGTACAATAAATTATTTGAATTTAGTTACCCCA TTGTGCTATCAATAATTCAATCTTATTCATTCTTTGTAACATAATTTTGTGTA
WI-21512	54 C G ---	---	TCCTGCTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAAATTTTCTGTC/G/TAGAGAGGA AAGAGCTGGTCCCTGCTCTGGAGGCAACGTCAGGTCGGGAAAGGCACCTGCTGCTGATCTGTC TCAGTGATGGGAGGTCCTCACTGCCCCACAGGAGCCTCGGGCCAGAGATGAGAAATATGCTGTAA TCCAGTACAGGGGCTGCTGCTGGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAAACTCTTAAGGCAGGACAAAGCAACTTTCCATT ATTCTTAGTTTAGACCAGAACTCTTAATTTTATATTCTCTTTTAACTGTCAAAATACACCAATA CTTAGAGGAAAAATTTCACAGTATACCAAAACATTTTAAAGATAAGAGGCAAGTGTAA/G/A/JAGTAG TATTCTACATACCACAGTATACAATGATGCTTCCCTGACGTTTAGGAAC

-268-

WI- 21514b	133 CT ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTCTAGGACTGGTCTATGAGCTGACAAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGC[C /TJACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTAAAGGTGATTGTGAAGGGTCATAAGGAACT
WI- 21514a	100 AG ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTCTAGGACTGGTCTATGAGCTGACAAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCA[AGTCTTCAAGGAAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTAAAGGTGATTGTGAAGGGTCATAAGGAACT
WI-22020	27 CG ---	---	ATGAACATGTTGCAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGATATCTACCTGTATGAGGGTACTT
WI- 19576a	113 AG ---	---	TTTCATCGGTTCTTAATACAGTACAATCCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTAACATT[C/AGTCTAGTTCAAGTATTAGT CACAGAAATTAACATCTGCCAGATGTACACAAATTTGGTAAAAAAGTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141 AC ---	---	ATACACAGGCCACAATTCAGGATGGAAGGAGTGGGCACTTGGAAAGTACTACACATGCGCAATA AGCAGCCTATCTCTTACCAACCCAGAGTTCTTGGGGCATGTATGGTAGGCCAGACCCCTTTCCAA GGGAATA[AC]TACTACACTAAGCCTACACTGTACTGTGAGAGTCAATGGTGAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTGTTCAGANITCTAAGGCCAGCAT
WI- 21574a	235 CT ---	---	AAACCCAGAAATTTAGGTACTTTTGTATTAGGAACTCACTATACTAGGAAGCAACTTATGAGTG TGTAATATTGATCTAGCAGCAACTTTCACCTGATCCTGGCAGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGCAGGCCAGGGAACCTTACTGCCTACTTCCCT[C/T]GTCTGTCAGGTGGGA
WI- 21644c	151 TA ---	---	TGACTGCCAAGATTTAGGCCCCAAGTTCAGGCAAGGTCACCTTAACCTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAATGGATTTTCCACCATANTATTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGA[T/AT]TCAATCAAGATCCATGGAAATGATGCAGTTTAACATGTGTCTCAGC TTGCCTACTGACCACTTTCCTTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55 GA ---	---	TGCTCTTAACTCAAAGTCCAAATAACATATAGACATTTTGANATAGCTATC[G/AT]TTTAAACA AACCTCATATGATCACTGTGCAATTCAGTCACCTAAAATACGGAACCATGACTATTAAATAAACA TTTACTGTGTGTGGTTTGTGGGACTGAACATAACCATACGTGTATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 CT ---	---	GACCGAGAAAAAAGTCAAGGCATATGATGTTTGTGCAAGTATACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACATATTAAGATAAGGATGGACT CTTTCAGTGAATTA[T/C]TJAGGACACAATCGACGGATGTAATCTATTGANTTATACCATAGGCCC TATTCATATTTGGCCAAAGGGAAGGTAGGATGGTACTGTGGAACGGGA

WI-21981	61 T A ---				TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAAT/AJGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAAATGCATGGGATAGA
				---	CACCTGTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTTATTACTTTTACATGTGGACAATCTAGTTGAGCGTTTAAAGGTTAAATTTGG
WI-21660	120 C T ---			---	TCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGGTGAACACGCCCTCTCCACTGCTTACTGTGTGTACCAAGAGGAGGAGGAGCTCACCCAGCCTAACCTGGCC/C/TJTGCTTTTTTCAGGCTTCAGGATGCCACAGCACATACTGGGGAACCTGGGATGCAGGAGAACCCAGGGTCTGTCTTCAGGAGGGTCACAGC
WI-19105c	211 C T ---			---	TGGAAAGTAGCCCTTCTGGACAGAAAGATAATTTGTGGTCCATGTGGTTGAGTCTGTTAAGAGGACACTAAGGCACATGGCTGGTGATCTTTCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTGTGTAGGTTTCCAGGCTGGGCACAGAGGTGAGGCGAGAAATNTGGGGTCCCAGTGGATCTCCCCACAATTCCTCCAGGGGAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-19105a	33 T C ---			---	TGGAAAGTAGCCCTTCTGGACAGAAAGATAATTT/CJGTGGTCCATGTGGTTGAGTCTGTTAAGAAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTGTGTGTAGGTTTCCAGGCTGGGCACAGAGGTGAGGCGAGAAATNTGGGGTCCCAGTGGATCTCCCCAACTTCTCCAGGGGAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-21760c	81 C A ---			---	CAACCTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGTCTTCTAGCTTTACAATAAGNGGAGGACTCTGACTGCA/CJ/CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---			---	CAACCTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGTCTTCTAGCTTTACAATAAGNGGAGGACTCTGACTGCA/CCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---			---	TCTGCCATATTGTTCCAGCACCACTATTACTGTTATTATTCTCTTTGAGGAAAAACAGGNATTAAGAAATCTGGTTTGAATTTCCATGATGCCTAACTGTTAAATCCTTTTCTTACCAAAAGGA
WI-20934a	72 T G ---			---	ACTTCTTAATCACCAGAGAAACAGAGGAGGAAAGTGAATGTTTGCAGAAATTTATCTCTAC/T/CJAGAGACAATTCATAGTTTCAATCTTTCAGGGTTGTGCTTTACTTGGGGGGC
				---	CCAACATGCAACATAGTCTTCTTAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCAAGAGAA/T/GJCTAAGACAAATGGTCAATATTCAAATGGCCTGGCCTAGTGGTAATCCAGCAGACAAACAGCATGAGAAAGGCCGGGAGACAGTAATAATACGTGCCCATGCAATGAGTTACCCAATCAAGCCCTTACCTCTTAAGATGGCAGATTAGAAGCCCTNTTCCCCAGGAGA
WI-21561	55 T G ---			---	TTTCCATTTTATTACGCCGGGCCATCAGAACATAGCATCTATACCTTCGAAACCT/GJ/CCTCTTAACCTCTCCCAGGCAAGAAAGGAAAAAGTGATCATATTGAATTCCTCAGATGGTGGGATCTCAAGACTTTTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAATATAATGATGATAATGGTAGCCCTTCTGGAATAATTTTGTGTAATCTGTTTAAAGAAATTTTGTGATGCATTGCCCCCA

WI-21961c	200 T G ---			AGCTTTGCTTGA AAAATTTGGTACTACTACCTTTGCAATCTCTTTATTTATTTATTTACTTTTATTT TTCCGTAAGTTATTGGGGTACAGGAGGTATTGGTTATATAAGTCTTTAGTGGCGATTTGTGTGATT TTGGTGACCCATTACCCAAAGGAGTATACACTGCACATACTCGGTCTTTATCCCTCGCCCTTGGC TCCACTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGCG
WI-21961b	73 G A ---			AGCTTTGCTTGA AAAATTTGGTACTACTACTCTTTGCAATCTCTTTATTTATTTATTTACTTTTATTT TTCCG/ATAAGTTATTGGGGTACAGGAGGTATTGGTTATATAAGTCTTTAGTGGCGATTTGTGTG ATTTTGGTGACCCATTACCCAAAGGAGTATACACTGCACATACTCGGTCTTTATCCCTCGCCCTC TCCACTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGCG
WI-21956	26 T G ---			CCCACTGGGTCTCTTTCAAGTGAATTT/GJTTCCTTCCTGCTCTAAAGCCCTTTAAATGAACCT TCCATTCTGTTCTGAAACTTGCCTTAGTCTGTTTCTGCTTCATGCCCTCAGTCGAATCTTCTCTT CTGAGCGCGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGTTGACGCGGTAACTCAGGGTAACCTC CTATCTTCCACCGGTAAACAGAGGGGTACATTATGGGGTCCAGGT
WI-21966	148 G A ---			CAAACATACATTATGGCTGCCCTTTATTTAAGAAATGTTTACTGAGAACTGTACTGTAAACAACATAT TTTTGTTAGAAGCATGAGTGAGAGTGTTGTGTGTGTGGCGCGCGGCATGGCACTGGCAGG GGATTGCAATGGG/G/AAACAGGATAAAAAGGTATAAAACTTGGTCCGAAATCTTTGCTTATTAAC CTTGGCCCTGCTCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---			TATACTGGTTTTTGGTTACATGGATGAATTGCTAATGGTGAAGTCTGAGATTTTAGTGTACCCATCA CCTGAGTAGTGTACATTGTACCCAACTGTAGGCTTTTATCCCTACCTACCTTCCACCTCCCCAT TTTGAGTCTGG/CATAGTCCATTATATCACTCTGTATGCCCTTGCATACCCATAGCTTAACCTCC
WI-21139a	165 T C ---			GCTCTAGTGAAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTCTGCCA CTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTGCTCTCTCTGTGAAATGGGTACAA TGTGGGTACGAGTAAGGAACATAACA/T/GTACAGCACTTCAGCACAAAGCCTGGGCACACAG CACTGCATGGAATACACAGGTAACTTTTAAACAGTGGGACAAAATTTAAGTACGTGGCCAGC TGTTGGTTGCTTGTGGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGTGTACA AATTTTGTCTCTTCAGTTTTTCATTAAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAA ACCATCATCAGAAA/G/TTATTAAATTAATTGCATATTTTGAGGCTACTCT
WI-20317b	217 G T ---			CAGGACTTGGTTGCTGTCCCACTGCACATAAATGTCCCTTTTGTGTGAGTTATGGTTGTGTGCG TTTTCTCTTTTGCAATAAGAAATATGTCCATTAGTCCAGAGGCTCTGCTTTATCCGGATGACGGAGG GTACACGGGGCGTCCGCTCAGTTCGCCGGAAGGAGCTATTC/G/ACTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAATCTCTTTTGTGTCGAACCTCT
WI-22082a	179 G A ---			

WI-22082b	67	C T	---			CAGGACTGGTTGCTGTCCTCCAACTGCACATAAATGTCCTTTTGTGAGTTATTGGTTGTGTC /TJTTTTCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGTTACACGGGGCTCGCTCAGTTCCGCGAAGGACGTATTCGCTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTGTGTCACACCTCT
WI-20993	139	A G	---			AACACAACTCCATGCTTTCAAGATTCACACACCCAGATACAGACATATTAAAAATTTACAGCAAT TAAACAGGTAGTTTGGTACAATAACACATATAGCAATGATACAAAATTAGGGGAAAAAACCCCTGG GCTTCTA/GJTAACAAGTGAGTATACATTAAAGACAGTATTGCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGCCTATTTCAGGCTTCCTAGCTCATCCACACATCAACC
WI-21723b	125	A G	---			AAGCGATTTTAAATGATTGGACATAGTGGTCAAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATCCCCA[A/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82	G A	---			AAGCGATTTTAAATGATTGGACATAGTGGTCAAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTG[A/JACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99	T G	---			CAACAGATGCTTGAGCCAAAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTGCCTTTTACTATCCTT[G/JCCCCATTTCTCTAATCTCTTTTGCTTACAA TATATTACCTTCTAGGTATCACTCATCTATAGGAATGCCTTCTAGTTTAAATGCTGCCCCCAACA ATACTAACCCATTGAAGGATAACTATGGAAACCTTTTAAATGGGACAGTGGG
WI-21008a	106	A G	---			TGACAGATCACACCACATTTGTTTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACACATGTGCACACAC[A/G]AGAGGCAAGTACAAAAATGTAACC CCACCAAGTGATGTGAATGAAGTGCAAAAAGGCTTCATTGCAAACTCTGAGGATCATTCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C G	---			CTGAGGCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGGCTTGGAAATAACTGAAAAGATTCTAT TTTCTCTTTGTGTACAAAGGATTCAAATATTTTACATCTCTCTTCTGCCAGTTAAACGTGCCGTGG CT[G]CAATACACACCACCAAGCCAGCGTAACCTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	G A	---			AATGAAAATGCCACCCAGAGTTAACAGCTTGCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAAATACCAGTGTGCAGCTTGGATTCCTCCATGAAATTAAGCTGTGTGTGCTACCTTGTACATAA CTCAGGCCACCTGAAATATCTGTAGTGGG[G/A]AATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATACCTACACATCTGCCAGGGTAAATAGGCATGGGCAAT

WI-21079a	50 G A ---	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGT[G]A[CGCAAAATCAAGT TGTTTTAATACAGTGTGCAGCTTTGATTCCTCCATGAATTAAGCTGTGTGCTCACTTGTTTACA TAATCAGGCCACCCCTGAAATATCTGCTAGTGGGAAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAAAT
WI-22129a	45 T G ---	---	TCTGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAAGT[G]TTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTTAACAGTTAACATTGAAGTCTTATACCTTATATTTA AATGTTAGCAATCTCTACTACATTTTCAAAATATAAAATATTTGGTTGCAAAATCCAGNAAGGGCA TTAACCAACATGGGACTGATCCTGGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79 A G ---	---	TGGAGTTAAGTGGGGCTCTGCTATTTCCOCCAAGAAAGACTCGGAAGATGTTGATCCAGGGCAGAGT GAGGGCAGAC[G]G[GGATGAGGCTCTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGTTGGGAGCCTCAOCCAGAGAGCCTCACTGCTATGACCCACACACCCACTCAACC CAGCACACAGGCACACGCGAGGCACACGCACACACGNTGCACTCACCAAGC
WI-18916b	42 C T ---	---	AATGGCATCCCTGTGATACCAACATCTTCAGCAGCTCAGC[G]TGGCTCCCACTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTGCCCCACTACTGCACTGGACACAGCCCTCAOC AATGCCACCTTCATA
WI-18916a	35 G C ---	---	AATGGCATCCCTGTGATACCAACATCTTCAGCA[G]CJCTCAGCCGGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTGCCCCACTACTGCACTGGACACAGCCCTCAOC AATGCCACCTTCATA
WI-19828c	200 A G ---	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCCAGGCTCTGGCCCCAAATCTGGGTTCTCCCCAAG CCCATGCTCTTCCACTTCTCACAATCTTACTTCTCTGACCTGACCCACCACCCAAAAT[G] JCTTTTAATCTGGAAAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 C T ---	---	CACAAGAGTCTGTACAACTTAGGGACACAGCCCTGGCCCTGCCCT[G]TAGCTGCATGCCACCCCTC ATATCCACCCCCATCCCCAGCCTCTGCCCCGACACCCAGGCTCCCTGCTCTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTGTATCCCAACCACAGCATCT
WI-19860	51 C G ---	---	TTGACCTAAGCCTAGCATAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C]GJCTGCATCAGTAT CTCCATCCCACATAATTTCTGTTTGAATTTTGCCATTACCCCATAAATGGTGGGATCTACCTCCOCT CCTTGCAAATTTAGCTGGNCCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19898d	80 C T ---	---	ACCCAGCTCCTTACCCTGTGGCTTTCAGTAGGCTTTGGCTAATGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGGG[C]TTACAGCAATTTATTCCTCTTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCTTGGCCACAGTCGTAACCTATTGC

WI-19891c	172 C G ---				TGTTGGTGTGAGAAITTCACAGCTTACTACAAGGAAGCTGAGAAATGCTTGGTGGCCCTCCCTCCCGG ACTCCTCTGTCTGGAAACGTGGCTTGNCTCCAGACACAGTGTGATGCCAGCTCTCTCAGCGG AGCTCCGATCCCTCAATTTGCCATCTGTCTGACTCQIGCTCTCCGGGGCGTGGGCGTCTGTGT CAGGAGCGGGCGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---				GCACCTGTAGGGGTGAGCTTCCATGGTTCTCCAGCAAGGGGTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGGGCTGCAAAACTGCTTTGAGGAAATNTCCCGAGGAGGAATAAACTAGAAGACGC ACCTGCTATTTACCATACTATGAGGAATACAGTAATGAAGTGTGGCAGAACTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTCTGTCTGTCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---				AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGCTGAGTACAAT ACATTTCATGTCAGGATAAGGAGCAT/GJACACCAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGGAAGGATGCT GGGTGATCTTGTTCCTCCAGAGGGCTGGGAGGCGGNGGGTGGTGGAA
WI-20270a	53 G A ---				AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCG/GJTCAGTGTAC AATACATTTCATGTCAGGATAAGGAGCATACACAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGGAAGGATGCT GGGTGATCTTGTTCCTCCAGAGGGCTGGGAGGCGGNGGGTGGTGGAA
WI-20622	130 T C ---				CCACTTCAATAATTTACAAATGCTCAGCAGCAAAATATGAAAAGCTTCAACACTTTCCTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAA[T/C] TACTAAATTTTATGATGTTACTCATATTTTATTCATATACTTTTATGACATCATTTGCCAATACATA CAATATTTCTNTAACTTTATTTTACAATAAGCCAACTCTGTCATGCAG
WI-20768b	190 C T ---				TTCCACTCAAACTCCACCCCAACCTTCTGGAAGGCGAGGGCTAACAGGACCTCTGCTGCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTCTGTATATCACCACTTA CAGGAGAGGTCTATTTCTGGGGCACCCAGAGNTCAGCACACATCTGCTGGGAC/TJCAGGGACTC GTAATTCGCTTGGTCCAACTCTCTATGGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T ---				TTCCACTCAAACTCCACCCCAACCTTCTGGAAGGCGAGGGCTAACAGGACCTCTGCTGCTGC TCA/C/TJGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTCTGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGGCACCCAGAGNTCAGCACACATCTGCTGGGACAGGACTC GTAATTCGCTTGGTCCAACTCTCTATGGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T ---				TGTTTGGCTTTGTCAGGACTCTACTGCTTTACATAAATATCTCATCTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAATAAGGATATTGTTGTCATCTTTAAAGAAA TGCTTAACATACCAAAGIATJAGTGGAATCAATAGAATAAAATATTTAAGCTTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACCTAAATTTATTTCTATGTATGGAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTTCTGGAACATATTGGAACACTTGTTTTTCATAAGCTGCTCAGAGT GGCACAAATCCCATCCATCTTCAGGCCCTTTTAATAAGGTCAATTATGAATCTGAATTTCTJAGJTTAAT ACTCTGGTGCAATTCATTTCACTGCAAAAGCAACTGGCACAACTCCTGCGGGTGCAAGCTCTCGG AGAACATCTAATAATTGAGTCTAGTCTGTGCGGAACCTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAGGATGAAATTTCCACATTTATTTNCTTTTATGTGAATAGAAATGGCAGTGAAGTGTCTATG AACTGAGGCGAGGAATGGGCATGGCGCTGCGGTACCAAGCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGAGGCATCATAGAAAAAACCCCTCAGCCAGAGTTAGGACATTTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCTCAGGCTCTGTTGTGTCJTTCAATTTGCAAAATAAAACCCA GACCGGTCACTTTTCAGTTCCTCCAGCTCTATTTATTTATGATTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACCTCACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GACGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGTTTATGGGCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGTGAGGACCTTGTCTTT CTCTTCCAACTCTCTCTCTTAGCCAGAACTTTGCGAGAGCCCCCTTNATTTCTCTTCCCTCTATTCC CCTCCTTCCCCAAATGTGCTAAGGTCCCAATCCAGACCCCTCCACG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTACAGCCATAGTGAGGTTCCCCATTTGCTCAGTACCAGAJAGJTTTGAGTAC GGTCGTTTAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---	---	---	ACCTTGCACACCTGCCATCCGGTGCCATCTCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAG GCTTGTCAACCAAAATGGGAGCTGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTT TCACTTGGGTCTAGCATCCAGCTCTCTCAGCAAGGAGGATTGTGGTCTJCCCTTGTGTTTCTG AACAGGCCCAAGGCGAGCCAAAGGCATGCCATCACTGCAGCACTCAACCCCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTTTGAATATTT GTAGGATGGATGAATTTGAAGTGAATTAAGTCAAGATAAAGGGGCAACTCTTTAATJAJAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCTTACCCAGCTACACTTTACCTTGTATCTATAAAGTGTATTTAGAGT AAATACATTTGGCTGTAAAGTCGJAJGATCAGGTGCTCTCCACCAAGCAAAACAAACTGCTGA AATGTGGCAAGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGNTGCGCTTCCAGGCACAGCCAGTGCCT /CCTGGATGGCATCAGCACAGGCTCCCTGCCCCGCCCTTGAAGCATGGCTGTGTGCAAGAT
WI-21342d	59 T C ---	---	---	ATTTTCCCTTCTGTGTTTCGTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGATJCTJGGAA ATCTGCATGATTAATAACATTAAACAGTTTCATAAACACACCCCATATCAGAGTATAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATGCACATTCTCCTCCTAGTT T

WI-	21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGAGTCCCTCTTTAGGCTTCAAGA TAAITGTGATTTTCATCGACCCAGATACTTCCAAGTGGAGCGGCCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTAGCAGACATTGCCTGTCTTCTACCCAGCAGCTGCTAGTGCACTT
WI-	21763a	135 T C ---	---	GA CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGAGTCCCTCTTTAGGCTTCAAGA TAAITGTGATTTTCATCGACCCAGATACTTCCAAGTGGAGCGGCCTCAGACTGTTCTCAGTCACT T/C/GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTTACCCAGCAGCTGCTAGTGCACTT
WI-	21763a	135 T C ---	---	GA CAGTCCATTTGAGTCCACAGTCGAGGGTGCACTTCTCTTTATCTTGCTTAAAGCCACTTGGGTAA[AC] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTGTCAGAAAGTCCCTGGAGGAGGCTTCTGG
WI-	22440	64 A C ---	---	AAAT CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC
WI-	22449	74 T C ---	---	TTCTTTT/C/GAAAAAATACACAATGGGAAGTGA CAGGTTCCACAGAGGCTTTTATTTCAGCCACTCAGGACCCCTGGCTTCTGCTCCAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGCGAGGAGCTCCCCACAGCC[AG]CCCCACAGGGTCTCTGTT TCCAAAGTCTGATGATTAGGCAAGACCTTCACACATTCACCCACTACTGCTGAGAGAGGGTGC ATGAGGAGGCTGTGTGGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-	21965a	112 A G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTCTTCCTAAAG[C/G]GTCTCTATGATCAGAC CACTCTAAATGTGGCTTTTACCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG
WI-	21687c	115 C G ---	---	AG AGCTTTTACAACAAAGCGAGGGTTTAAAGAGCCTGAGAAGAATTTACAACACTATTGACTATACAGAG TCTTCAATTCACAAACAGTTAATAGTAACCTTGGTGGCAGATACAACATGCATTGAATCTCTGTAT
WI-	22374a	149 T C ---	---	TATTCAGTAACTAAAT/C/JAGGNTCCTGCATCTCTTCACA ACTGTCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGTTATTATGGGGTCTCTGCCTCTCTGGCTGTGTTATG[C/T]
WI-	22250b	132 C T ---	---	GGANCCAGGAGTGGAGGAGCGCTGGAATAGACAGGGGAG ACTTGCTTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGTTATTATGGGGTCTCTGCCTCTCTGGCTGTGTTATG
WI-	22250a	89 G A ---	---	GGANCCAGGAGTGGAGGAGCGCTGGAATAGACAGGGGAG GCAGCAATCCTCTCTCCAAACCTCCAGGCCACCTGGGGCCAGAGCACTCATGCCACAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCCAGGTTCTGGCTCTCAGGAGCTCCAGCAAGTGA GCCACAGAGTTTCTGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAGAACCTG[C/G]JAGTCTTC
UTR-	04932-2b	192 G C ---	---	TTTGACGGGGCGCGGTGCTCAGCTGCTCTCTGGGAGGTGAGGAGGGT

UTR-						GCAGCCATCCTCTCTCCAAACCTCCAGGCCACCTCTGGGGCCAGAGCACCTCATGCCCCAGCAGCAC
04932-2a	149	CT	---			CTACGTGCCCCGAGTACGGACCCGCTGGCCCCAGGTTCTCGGCTCTCAGGACGTCCACGCAAGTGGA
						GCCAGAGGTTTG[CT]TGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAGAACCTGGAGTGCTTC
						TTTGACGGGGCGCGTGCTCAGCTGCTCTCTGGAGGTGAGGAAGGAGGT
stFIBBb	412	GC	---			GTGAGGAAGATGGACCTGGACAGACAGTCAAGCTCCACACCTTGGCGTGAGCAGCTGTGATTGTGCCA
						CGGGAGCATGAGCCCTTTCCACAGGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG
						TTTGACACAGCTCGAGTCTCCATGTTGATGACATTCTCAAGATGCAGCCAGGAGCCTCTCTGA
						AGGACCAGTCTGTTACGATGGTCTGAGCTTCCTTAGAACCTTCCATGGTT
stFIBBa	341	TC	---			GTGAGGAAGATGGACCTGGACAGACAGTCAAGCTCCACACCTTGGCGTGAGCAGCTGTGATTGTGCCA
						CGGGAGCATGAGCCCTTTCCACAGGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG
						TTTGACACAGCTCGAGTCTCCATGTTGATGACATTCTCAAGATGCAGCCAGGAGCCTCTCTGA
						AGGACCAGTCTGTTACGATGGTCTGAGCTTCCTTAGAACCTTCCATGGTT
stIGLV2	61	TC	---			GTGAGGAAGATGGACCTGGGACGCTCTCGGACGCTCTCCACCATGGCGCTGGCTCTGCTGCTCAC[CT]CTC
						CTCACTCAGGACAGGTGACGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGGTCT
						TCCTGCTCCTCAGGCTCACGGGGCCAGCACTGACTCACTGGCATGT
stSG1001	70	TC	---			GTTCAGGCTCATCTTGAACCTCCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTGTCTGGGAT
7c						TA[CT]CJAGGCATGAGCCCCACACCTGGACACAAATACATTATATCTCTAAAGTATAGGATTACT
						TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1001	33	GA	---			GTTCAGGCTCATCTTGAACCTCCTGGTGTCAAGCG[GA]ATCTCCACCTCGACCTCCAGGGTGTCTGG
7a						GATTATAGGCATGAGCCCCACACCTGGACACAAATACATTATATCTCTAAAGTATAGGATTACT
						TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1002	63	AT	---			TAATGATAATTAGGCACTTCTCCACACGAAGATGACACAATTGACCCCAATATCATTTGAGGCG[AT]
3						AACAGTTTGGGCTGTTTTCAGTAGTATGACAGTGA
stSG1009	36	GC	---			GTGGAGAAAGATCGTCTTCTCCTCCCTCCCATGACG[CG]GGCTTCCCGCGGCACCTGTGCGTTTCC
6						ACCCGAGACGGCCTTTGTAGGGACCCACTGCCCCACTCGCTGTGCGCTGGTTCCGCTCTAG
						GGCTCGAGTGTTTAAG
stSG1011	107	CA	---			TAGGCTTAAACCTGGAATCTACAAGCCAAAAGTCCCTCCCTGCGCTGAGGGCAGTACCCCTCCATTGGGC
8						ACAGTCCAGACCCAAAGTCAAAGATGCCGATTCCTTGG[CA]CTCAGCCCTCAGTTCCTTCATTCC
						ACCAGGCCGTGCTTGTGAGTTTCTCCTCCAGTGAG
stSG1012	89	TC	---			TAGTAGGTAAGAAAAGCAAAGGAGGATTGCTTATCGGATGACTGTTTACAGTGGTGTGACACTATGC
0						CGTGTTCACGAACACTTTAATAT[CT]GTGTGTGTAATCTGATTATCTCTGCTTACAAATG
stSG1017	42	CT	---			TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAGTCCG[CT]GGGAGGAGAAGTGAACAGGAA
8						TCGATTCTTTGCTTTAACTGCCCTTAGTAGGAGATGTTTAAATACTTCGC

siSG1019 3	136 GA ---	---	GGACAATACTACCTAAGGACAAAATACTATTATTAATAAAAAAGTCTTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAAACATTTTAC TTG/AJTGTGAAAACGTGAGATTTAAGTTGCAAACT
siSG1020 2c	143 GT ---	---	AAGCTAACTTAGGTGAATGGTGCACCTCAAAGGTCTTTCCGAGGGAAGCTCAGTCTGGCTTGGCGAG AGTCAGCCTTGGTCACCTCATACCGGGCTCAAAGCTAAGCGTCAAGGAAGCAGTCCACTGCTTCT CGCTGCA/GTCAAGACCACAAGGCAGATGCCACTGCTGCTCTTTCCCTTGTCTACTTCT
siSG1020 9b	75 AG ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCAAATAAACTAATTCCTCTTAAGATCCCACATTTAT TTTTTA/GJCTCCAATAAATGTAATTATCAGCTGCTGAATT
siSG1020 9a	34 CT ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTC/AAATAAACTAATTCCTCTTAAGATCCCACAT TTATTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
siSG1021 8	29 TC ---	---	TACTAGACATGCAAAATGAGAAGATTACATTC/CTGTGAATATTTAAAGAAGTTATATTTGTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATCTGA
siSG1025 2	108 AC ---	---	ATAGTTTCAGGAACAAAATCATTAAATGGAATAAATGAGAAGAAATCTTTATTTTGGACCAATTTT AGGCACTTAAGAGTTTCTTCTCTCTTCCCTTGATCA/CJAGTGAAGATATGATAGGGAATTC AGAAATTCCTCTCTTG
EST10915 0	123 AC ---	---	CTGTATTAATTAAGAAGGCACATTAATGAGGGACGGAAATCTACCTGTACACAAAAATCTGTAC TTTAACAGCATCTTCAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG/CJATTTTAA GAACTGAGTTATTTGGAC
EST11023 1	166 TA ---	---	TTTTTGTAAACCAACCCCTGAAAGTTCCACATGTGAATATAGATACACAGTGAACAAAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAACAGCAGGGC AATTAGTCAATTAAAAAAAATAGTACATGTTA/TJAGTGTATAAATAAATTTTACAAAAGGCTTT TCCACTCGTGGATTGATTCCTTTTGGAGGGGAGTAACTCCTGG
EST14096 8	71 GC ---	---	GGGATGTATATTACAGATAACACAACCTACAATAATACCATCAGACATTGAAAACTAAGGCCATTCT GTGA/GCJTATTTTAAAACTTGGTGTTTTGCACATAATGATCTTAAAAAAAATGAATACCAA ACCAAGATTCTCTTCTAAATGAAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 CA ---	---	TGCAAAATTGTGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTAGAAATGTAGGTCG CAGGGATGCTTAAGTCTTCTCTGCGCAGAGACCCGAGGTGCAGAGATGATTTCTTCTCA/CJCCCTTC TCTCAGGGTCTGGAG
EST22555 7	60 GA ---	---	TCAAGCATGTGTAGGCACTGCCCCGCCAGACCCCTTCTAATCTCTGCACACTGGAAGGTG/AJAA CCCTGGGAGAGAGAAGACACTCCCCCTCCCTAGCTTCTACCTGGGCCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

EST22917 6	74 CT ---			GTAAACCTTGCAACGCCATGCTAAATGAAGCCTGACTGACCAGGGGCTCTTGGGCTCTCAATGCA ATAGAAAC[CT]TGACATGGGGCCAAAGACTTCCAGACAAAGCAGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTGTGA
EST36458 6	65 AG ---			CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCCCTCAGGCTGTCTACTCA[AT] GTTGTGTTTGTAGCTCAGCTGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAAGTCACTCTCCA GAGGGGAACTTCAAAGAGGATTCCAAACAGTGAAGCAGAAATCATGGGGCAAAAGTCA[AT]GTATGG GGCAGACTGAGTTGGACCAACACAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCGGC ACAGCACGGAGTAGCCAT
EST36745 3	56 AG ---			TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGTATG TJA/TJATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410c	201 AT ---			TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATG/TJGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410b	139 GT ---			TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCA[CT]TTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTT GGAATTTATGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410a	48 CT ---			TATGTGGGAAGTTCCAACTCATCTATGCTGCTTTTCTACTGCTAATATTGGATGCTTCTTGCCA GGCTC[CT]TTAAATTGTGCTGAACCTGGGAAGAAACCTTCTACTCTCCACAAACCTGAA CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGATGGTGAAATGTTCCGGACCTAGATA[CT]GTGACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR- 04350	125 CG ---			GAAATAAACTAAACTGCAAGCAATCACTGTTAATAAGAAATTGTTCTTGT[TT]C]GACAGTTG AAGTGGGTGTGAGATGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCTCAGATGCGGGCAAA CTCCTCTGTGAAAATGTAT
siSG1026 6	55 TC ---			GTATAATTCAGCATAAAGCCAAAGCCTTTTAAAAAACCATACTATCATTTTATGAAATCTTTTACA AGA/T]G]AAGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
siSG1028 2	70 TG ---			CACTTTAGATATGAGGAAAATGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAACCATGTGTTTGATATGCAATAACAGCAATAATTTTTCACCT[CA]TTG TCAATGCCAATGCATTGAAGGCCCCAGAAAATGAGAAAAGGATAACAAAACCTTTTGATAAAAAAGGTA AGAATTTCTGTGTG
siSG1031 0	128 CA ---			

stSG1033 1b	116 T C ---	---	TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCAATTCGG GCTCCAAACCTGTCTAGGAAGGCTAGACCTCAAACACACCTCCATTCGCAATTCCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---	---	TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCAATTCGG GCTCCAAACCTGTCTAGGAAGGCTAGACCTCAAACACCAATTCACCTCCATGCAATTCCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1243 b	225 G A ---	---	ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAAATCCTCCTCTTG AAATTATGTTACGGCCAGCATGGTAGCTTATGCCTGCATCCAGCACTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGATTCGACACCAAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATCTGTTTCG/AJAAAGTATTTTCAGACCAAAAAGGAGGT
stSG1345 b	60 G A ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACCTAGTTTGTCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGTCATAAATGGGGCAA
stSG1345 a	54 T G ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACCTAGTTTGTCTTACGGCT TCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGTCATAAATGGGGCAA
stSG1385 b	117 T G ---	---	TTAATGTCATCCAGGGAGGGGCCAGGATGGAGGGAGGGTTGAGGAGCGAGAGGCAATTTT TGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTGT[G/T]CAATCATTAAGAA GACAAAGGGTTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGCTCTTAAANACATGGCC CCAGCAGCTTCAGTCCCTTCTGTCG
stSG139	69 T C ---	---	TCGTCTCCTTCCAGTCTTCTGCCAGAAGCATCCCCATGATTTGTGACCGCACAGCACTTTGTGTCT TTCGCTTGAGCACTTGCCACTCTGGCTGGTGTGCTGCTGCCACTGATTGTACTGTCTTGCTGCOO GATCTGGTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTTGTCAATCCCT TGGCTCCTCCACTTCCAGTTGGCTTCTGCTCCTCATTCAGTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGCTCCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGTCCTACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103 T C ---	---	CCCTGGAGTTCTGAACATAGGAAGAATGCAAGTCATGTGTAGGTCC[G/G]CTCCCTTGCATGA AATGTGGGAGAGGGAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---	---	CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGTTCJTTTAATCAAGGTTGAGA ATGACGAATTCAGAATTTCTTTCATACATAAATGCTTCTCCTAGTTCTGCAAGATGGGTA
stSG1483	44 T C ---	---	CACACCCACAAGTTTCATGCTAATGCAAGTATCAAGTCTTGAGGACAAGGCAAAACCAAGTGTGCA TCGTAATGTGGAGGATGCTGTTGACGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAGAGGAA AATGCTCTGA
stSG1696	67 C G ---	---	

siSG1847 b	95 GA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAAATTT AGAGGTTAAATAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATGACTGTGCT TCAACACAACTG
siSG1847 a	49 CA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAATGAAAGA ATTTAGAGGTTAAATAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATGACTGTGCTGC TTCAACACAACCTG
siSG1897 a	83 AG ---	---	CTTAATGCCCTTCCTCTCTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGACACAGGACT[G/G]GCCACACCTCTCTCCGGTCTCCCAAGATGACT
siSG2022 a	86 TC ---	---	TGCTTTGAGGTTTCAAACTCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATACAT[C/A]ATTCCATAATCTCATCTATTTAACATTAAACAGGCCCTTTGTTGT TGTTATTTTCTCCCTACAATATTTCTGACTCTGTAGGGACAGTGGGCTCAGTTGGGGGTTGAC T
siSG2076	104 CG ---	---	AAACGTTGTCCCAAAATTTGTTCAGTTTCAAGATATAAAATAAGACTTCTGAAAAAAAGTTTACA ATTAGTTATAAACACCTTAAGAATATATTTGACATT[C/G]ACATCAGATGGGGCATTTT
siSG2108 c	71 AG ---	---	TTGAGCAACAATGATTCGCGAATTTGGCAGCTCCAAACCACAAAATGATTGAGGGCTCCACAGAGA GAGC[G/G]TAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGTCTGA
siSG2108 a	49 TC ---	---	TTGAGCAACAATGATTCGCGAATTTGGCAGCTCCAAACCACAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGTCTGA
siSG2141 b	173 AG ---	---	TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGAAATAATCTCAGAATGGCAGCACCACTGGCATGGCGATGGTGCAGGTGGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[G/A]AGTTCCCTATTATATATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTGTCTGTG
siSG2141 a	113 CT ---	---	TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGAAATAATCTCAGAATGGCAGCACCACTGG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGAAAGTTCCCTATTATATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTGTCTGTG

-281-

stSG2148	50 A G ---	---	---	TGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTC/GJAAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGCAGGCTC ATCAC
stSG2175	68 C T ---	---	---	CTCAATGAGGACTCCATCAGCCAAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGTGCT [C/T]GCCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACCGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGAAGGGAGTGAAGGACCA
stSG2189	41 C T ---	---	---	CAAGTGTGAAAGCTGGGATTGAGCCTGATATTACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACTCATCGCTAACTTTGAGCACTTAGTGTCTGAGTACTTGTATAGGTTATCTCAATCCTACTC CAGCTTGGGAAC
stSG2200	49 T C ---	---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGTTCTGTATGATG[T/C]TTTATATTATGTAT AATGCTTACCTGATGATACCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	---	CATTTCTGCCTCTGCTCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G/T]AGAGCATCTCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
stSG2257	65 A C ---	---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGTCTAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[J/ C]CTGTCAGGAAGTCTCGCCAAGCACTGGGCTGCTGCTCAGGCGAGAATTTCTTCCT
stSG2306	67 A G ---	---	---	GTCAACGCTGAGAGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGGAACTATTTTACA [A/G]ATGCTCCCATTTGGGTTTCCAACTGATACAACCATGAGGTGAACACTTTCACCTGTTTCACAG TTCTCCAGAGA
stSG2334	70 T G ---	---	---	GAAACTACCCACAGCATCATGTTAAAGAGAGAGATGAAAGAAAAAATCCCCGCAAAAAACA AAAAAT[G/T]GCAGTGGAGGGGCTGTGGAGGGGTGAATG
stSG2339	63 T C ---	---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGCTTGACTGCAGAAGTAAGTGTGTCACT[T/C] GTTCTCAGAGTCACCATACGGTGACTGIGTCTATTCTGGCTGTGCTTCTTCTATCA
stSG2465	76 C T ---	---	---	CAAGACTAAGAAGCCGACCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTCAAAGTGTGGGGTATGCA
stSG2549	140 T C ---	---	---	TTGCAGGCTTGTATTCACAATAACAAGTCATGTATAGAGAATGTGAAATGATACCTTGAAACCAA GATATAAAAATATTGAAGTCATTTATGCCCTTTGATGACTGGGTTAAATATGCAAGCAGCTAAAG GAATAT[T/C]TACACACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	---	AATTGCCAAATGGAAAAATCCAGAGGATTTTAGACCAACTTTTGGCCTGTGTGCTTCCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA[T/G]GAACAATC CCGGCCCCAGATTAAITAT

stSG2577 a	121 C T ---	---	AATTGCCAAATGGAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATCCAGTTTGGT CCCAATATAGGCCTTCTGCAAGAAGAGATCAATGCCGAACCGAAGCTGTGAAAGC/TATGAACAATC CCGGCCAGATTAAATTAAT
stSG2700	58 G A ---	---	ATCTCTCGACTGCTTTAGTGGGAAAGGAATCAATTTATTTATGAACCTGCGGCCCC[G/A]AGTCAC TCAGGTTTGGGGAAATAAACCACTGTCCAGAGAGAGGAGGCTACTTGAGCCGGACACCA
stSG2724 b	101 T G ---	---	AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTCTTTATTAATATTTGCAATGCTATAAT TTAATACTTATATCCAAATGCTTGCAATCA/TG/TJTTTTTAATCCTGGGTGTTGAAAGAAC GTGGCCGATCTTTACTTTTCCAGAAAGCGGTAATAAATAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCAACAAA ATATCCACTAATTCGCCAATATAGTAACCCGTGCTTGTCCGAATG
stSG2776 a	65 G A ---	---	AAGGAAAGGTGGAGGGAAGAGGAAGAAATTAACAATGTTAGAAAAGAGCAACTAAAGATTATTC TATTACTTCTGAACGGTAAGTAGCAATTTTAATAATATTG/TJGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 b	109 G T ---	---	AAGGAAAGGTGGAGGGAAGAGGAAGAAATTAACAATGTTAGAAAAGAGCAACTAAAGATTATTC TATTACTTCTGAACGGTAAGTAGCAATTTTAATAATATTG/TJGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100 A G ---	---	CCGCAATTTTCAACACACATCTATGAAAACCTAAGGGTGGATCATGTACAACACAAAAACAAGC TCCCTCCCTCCAAAACAA[C/T]GAACAAAAATAAAGAAAGAAAACCCATGAATGCCAGGTTTA ATTTTTTCC
stSG2826	85 C T ---	---	ATGGGTGCATTGTAAAGGCAATTAATACTTTTTCAGGCGGGCTGGCAAAATTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCCTCCCAT
stSG2850	88 G A ---	---	ATACTCAGGGGGCTGAAGGCAATGTGAAGAGTGACTGCAAGTCTGGCATTTTCTGTGGTGCAGC AAAT/C/GCCCCCTTATTTTAAATGATTCCAGACATCTGGCAGCATAGCT
stSG3031	71 T C ---	---	GTCCCAACTCTCTCCTCTTAGAGAAAAAAGTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAGCCAAAAGGCAAAAGTGGTGAGGC
stSG3058	81 G A ---	---	CAGCATCTCCAGAACATCTCTAGAACTGAACCATTTCTGTCACTATTGAAAAACAAAGCCAAAGTTT CAATCCAAAAATAATAATGAACGTGC/T/GIGATAAACATTTCTTATGGTTCCAGCCCCCTACTTT AGTT
stSG3092	94 T G ---	---	AAGAAGTACTTTGGTAGCTATTTAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACTG CATCTTTAGTCAATTTGCAGTGGAGTCA/G/GTGGGGTGTCTAAGTGTCTGAACTGAAGTAG
stSG3230	95 A G ---	---	ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTAGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTAGAGGCCAGTGGGGTGGCCACTTGGTGTCTTCTACCAACCCCTGCGCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGTG/G/CTGTACTTGGCTTAACTTCACTTCACTGCTTTAT
stSG3245	160 G C ---	---	

siSG3265	42 TC ---			AGGTGAATGAGTTACTAAATGTAGCATTATTTATAAGGAA[TC]GCATTGTGAATAGTTCTCAG TTTTCAATTATGGAAGATGATGATTCAGCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTTCAGTACATGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGCTTGTCAGCTGAATTTCTTGGGCTTATGTGGCAGTGTGGTAAAA
siSG3269 b	141 CT ---			TGTACTACTGTGTCATCCTATCCATTCCCTCCCTGAGCCTGGACTGCTCTTCCAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACOCCTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[CT]TTGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAACT
siSG3269 a	24 AG ---			TGTACTACTGTGTCATCCTATCC[AG]TTCCCTCCCTGAGCCTGGACTGCTCTTCCAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACOCCTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAACT
siSG3284	130 CT ---			TTAAGTCAAGAACTTTTCAGTTACAGGAAGATTTATCTAATATAAATGACTAAATACAAAAAGC ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCA[CT] TCCCTAACTTTTGTAAATGCTGTAAATGGGACATTTGTTGTTTGTATCTACCC
siSG3292	99 AT ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAAAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA[AT]TACAAATCAATAGCATTTTCTAACTTCAA TAAATGTCATATCTTAGCTCTCACT[CA]CCAGTGTATCCATTTTCCCGAGCGTAGAGCTTTCTG TTTCTGTAGATTGCCTGCTCGGACATTTGATATAAATGGAGTTGCTGTATCATGTTCCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCACTGCTTCATTCCTTTAA GATCCCCAGTATTATTTCTAAATGAACTTGTTGTGGAATAAAAAATCTGAGGACCACCTCAGAG GG[CT]ATAAGGGAACCCCTCTTTGCTTAGTTTCATAAGGACTTTCT
siSG3369	69 CT ---			CAAGACTGTAAGAACGTAGGCCTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAGGAATGACATTTCCAAACTGTACCTTTGTAGC[GT]CTGGGT CAAAGTCTAAGAGGACAAATAATAGAGACT
siSG3398	125 GT ---			TCCTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATACG[AG]CTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTCCACCTCAGCCAACTGAGTAGTGGCCTGCAGGACAAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
siSG3416 a	43 AG ---			GTAAGACAAGGTTTGTCTATGTTGACCAGGCTGGTCTTGAACCTCTTGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCCCGGAGCTTTTAACTGAAT GTTGAAATCATCTGCTCTTTGCTGGGTAACACTGAT[AT]CAAGTTGCTTAACCTTTGTGAAACCCAC TTTCCCTTATCTGTACAAATGGACAACAGAACTTTTCCCTTCTCTC
siSG3424	173 TA ---			GTTTCATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTCAGGTGATGTGATGGAGGCCTCACAGA ATGAGTGGCAGAGAGGGGCCCTT[AGAAATAGCTTACTCTGTTTCTCTATC
siSG3436	88 TA ---			

siSG3463	103	C T	---				GATACAGAAGATAGTGTGGTATGGATGGATAGTATGAAGGACAATAATACAAATATATTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTAC[C]TJTGGAACAACTTGCTTGACTATATTA CTGA
siSG3491	71	G A	---				CAAGATACTTCATTGCTCTAAGTAGTGCAGTGTGGCAATAATTTCTCAGCAACGAGCATTTTG AAGA[G]AGTGGAAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCACCTGTGGATTTCTATAAACCTCATTTATCTTTCTGTGATG ACAGAAAAATAAGTTAAC
siSG3523	33	C T	---				TAGCCATCTTACTCTAGTTCCTTTTGGGTTTTA[C]TGCAATATATGTGTACAAACACACACACACC CCTAATTCCTCAATGCTCTTGGCATAAGTTTTATCTCTACTGGTCTC
siSG3536	213	A G	---				AGTACAAACACAGATTAAAGAGCTCAGCAGTATTGACACGCTGGAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCTACCTACACAGCTGTACAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGTGCTGAAACGCATCTCAGTGTCTATTGTTTATTTGTTAAATGAGCTTG TGCACCATTAAG[G]GTTCTGCTGGGTGTTCTCAGTCTTGCCATGGAATG
siSG3583	112	G A	---				GAAAAGCTTAACATACGATCCATGTGCAAAACCCAAACAGGATCTCGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGACATCCACACAGGCAC[G]A[TAACATACACAGTACTGT CTAGTTATCAACACTAC
siSG3586	60	G C	---				CCTAGTAACATAGTGAGACCTGCTCTCTACTAAAAATTTAAAAATCAGGTGTGGTG[G]CJACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
siSG3589	101	T C	---				ATATAGTGTGGTAGCATTATAAATCCTTTTAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT GTATATACCACCCCTGGCACAAAAAACCCCAATGA[T]C[CCTATTTCCAGAATGTATCCAGATGAAA GTATCCAAACAACAAAAAGCTATATACAC
siSG3590	70	A T	---				GAGAGATGAGCTATTATCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTCTAAAAAAA AAA[T]TTTCTCTGATGTCTCTGACCCCTGTAGGAAACACATTGATTTCTACACT
siSG3619	78	A C	---				CAGTGAGACTTCTCATTTTATAGCAAAATACATTTTGCAGCTTAAATTTCTTGAATTCATACGCT TCTGTCA[T]T[A]C/AACAACCTTCCAGAGAAAACTGGGCTCTATATATTTAAG
siSG3644	40	T C	---				ACATATGTAAGTGCCTAGTAGCCATATTTAGGATGAGAT[C]GGATTGAGAGGCATGAACCAAGG ATCGGTAATAATCATTAATGAATAATAAGTTATCTGGGAAACGGCCATTGTCCCAACATTACTAA GTGCCTACTA
siSG3646	70	G A	---				CTCATAATTAGATTGAGATTGTGCATTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G]A[ATATTAAGTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCAIT CTTCTCTTTGTA

siSG3646 b	55 A G ---			CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATA/GJ/TATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3646 a	43 A T ---			CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATG/A/TJGATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3693 b	85 A C ---			ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAAACCCTGGACTCACCT GAAATATCCTACGAGG/CJ/TCGCCCTCCGAGACTGACGATTATTAAACCCACACGGGAAAAAGG
siSG3693 a	30 C T ---			ATTGTTTCCCTGAACATTCCCGTGGTCTCC/CJ/TJCTGAAAGCCGATGACCATCCAAACCCTGGACTCA CCTGAAATATCCTACGAGGATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGGAAAAAGG
siSG3698 b	145 G A ---			TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCAACCAATCCCAAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG/G/AJAGAATACCCACCCACCTTCCCTCACTGCAGA
siSG3698 a	51 C G ---			TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCAACCAATCCCAAGGTTG/CJ/GJCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAATACCCACCCACCTTCCCTCACTGCAGA
siSG3724	107 C T ---			ACCAGCCTCATGTGCAGAGGTTCTCCTGCTGGATCCCAACTGGAGCCATCCCTGGGCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG/CJ/TACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
siSG3725	104 G A ---			GCCAAAAACAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAAATATATTATACCAGCCAACAGCAAAACAGCCC/G/AJAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
siSG3751	128 G A ---			CGGAAGAAAGAACACAAATCCACAGGAACAATCTATGGTTTATACCTTTTGTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGGAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC/G/AJTT GCTGACTCATGTGTTGCAAGAG
siSG3787	49 T A ---			TTCTGTGCAAAAGAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTA/T/AJAAAGTCCCTAAGA CACTGAGGGCATAAACCACAAATAAAATAAGGAGTGTAGGCTAAGCAGATATCTTCCCCT
siSG3880 b	115 G C ---			GACAAGAGGGAGAGATGGCCAGAGACCAAGGCTGGGCGAGCTGGGGTCCCTGAGTGCCAGGGGC CACCACAGTCTGTGGGTCAAGGCCCTCTCTCTGGGAGCAGGTCTA/GC/JGGCAGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTCTTGCCCT

siSG3880 a	36 GC ---				GACAAAGGGAAGAGATGCGCCAGAGACCAGGGCTG[C]GCGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGAGCAGGCTAGGGCACGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGACCCAAAGAGTCCATTCTGCGCT
siSG3895	44 A G ---				AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTG[C]A/GTJTJTJTJTJTJTJTJTJTJTJT TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATTGGGAACAAGATGCTGATTCGTCAACTG AAAAAT
siSG3902	104 T C ---				TCGTGTGAGACTGGAGAGACCAGGTACCAAGCACCAGCTCTGGTGGGAACCTGGCTTCCCTGATAACA TCATCTATTTACACTAAATGTGAAGTGTCTTTCTTTCT[C]T[C]CAGCTCAATAGCTTAACATCTAATTC ATGTTTGTCTCCCTTTGCTGGACAAT
siSG3935	50 G A ---				GGGTGTCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[C]G/AJCTAGTGTGCAGGC TCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCTGGACGT
siSG40	25 A G ---				GAGGAAGAGGTTGAAGAAGTGTGA/GA/AAATATATTTAAGATTTCTTTGGGGAGAAATCTGTGTC CCAAACCTGGTGTGATGGATCCCTTACTATTTAGAATAAGGAACAAATAAACCCCTTGTGTATGTATCA CCCA
siSG4009	32 A G ---				GTGTGGGTGTCTGATGATGAATGGCGGCT[C]A/GTACTCTTTACGGTCTTACACTTTTATGTCCTCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGTTTTCACACTGCTTACA
siSG4033	123 T C ---				AGAAGCCTTGGGGACAATGGCAGTGCCTTCTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTTAATGTTTCAAGCATAAAGGTACTTTT[C]TGTGAAC AGGTGGGCAACAC
siSG4038 a	29 G A ---				GCTGAGAGCACGTGTACAGCCACGCTGT[G]A/PCGAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTTCCGGCTCCGGAGAGCAGCTGAGGGTTCCATCACT
siSG406	53 T C ---				ACTGTGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAT[C]G/GGTTTTAGTT TTGCTGAAGACTGGCCTTATTATGACAGCTTCTCTAACAGAGATTATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55 GT ---				ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGTAGATGTATTAG[C]TATAAAAAA GTTTGCTTCTGTAACTATTTAAAGCTTGCTTATCTCATCTGTAAACCTATGIGTCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4095 a	27 A C ---				ATCTGGGCTGAATTAGTCAAGCAGGTC[C]A/C]GATACTATTGTCTGTAGATGTATTAGGATAAAAAA GTTTGCTTCTGTAACTATTTAAAGCTTGCTTATCTCATCTGTAAACCTATGIGTCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4120	65 G A ---				TGCATGTTCCACATCTTTTATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[C]G/ A]CTTTTCCCTCAGAGAGCCACAGTTAAACAGCTTCCAGCACACCATTAATCCACCGAGCT

siSG4128	54 A G ---	---	CTTGGCAGATAAGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCTTGAJATATATTT TACTTCTCTGAAATGCGACATAATTTGCAATAAATGATTCACTCCTTAGCTCCAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
siSG4209 b	128 GA ---	---	CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGCGCGGCACCTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGCGCGCACTCCCTC[G]A/GC AGGGGACCACGAGGCGACAGGTCTTTGATGCTCCGAAAGCTGAGCTCCATTCCA
siSG4209 a	65 GA ---	---	CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTACAACATCCACATGGCACAAG /A/CAGGGCGCGCACCTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGCGCGCACTCCCTCGGC AGGGGACCACGAGGCGACAGGTCTTTGATGCTCCGAAAGCTGAGCTCCATTCCA
siSG4254 b	31 GA ---	---	CATTACCCAGAACGCCATGGAGGACCAGAGC[G]A/CACGGCGCGGACTCCCGCGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCGGGGGCTGCTCTCCCCCAGGGGCGACGCTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTCTG
siSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCAT TTAAGCAAATAAATT/GIAGCTTCTGAGTAGTTGTTCCAGTTTACCCCAACATTTTG
siSG4331 b	71 T G ---	---	CTCACAAGGCCAACACAGAAAAGATACAAATACATTATCCAGCTAATATTAGTTTATGACAC AGAGT/GITTTCAAACAAGTTTAAGTGTACCTGAAAGCATGTTAAAAGTTTAAGTTATCACTT GGAGAGCAGATTTCTTGGCTCGCCCTTGATCTGTTTGAGGGGTGTC
siSG4340	76 GA ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAACC ACATGTTCTC[G]A/TAAGTGGGAGATAACAATGTGTACACCTGGACGTGGAGAGCAGAA
siSG4361 b	109 A C ---	---	TTCCCAACCATTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGC/CJCCCTTCACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTGAGG
siSG4361 a	24 T C ---	---	TTCCCAACCATTGAGTGACAGAGCTC/CJAGTCAATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTGAGG
siSG4376	73 A G ---	---	TTTCACTGCTACTGTTTCGGTGTCTGAGTCTCAAACCTGCTTTCAGAGTCTTCTCCAGGGGAG AACAG/GJCTGGAACCTCGGCTCTGCAAGAGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
siSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAGATGACAACATACGATTTCTT/CJTCAGTCTTGTAGT ATCCACAGTAGTGTCTGTCCTATGTAAGTGTCTGCCAGAACCCCAATTAAATCCATGCC ACCAATGGTTCTGCTATGTGATCCGATATTTTGGCCGATCTGAATACTGCAAGGGCTTAACCAT TCAAAACACCGC/GJTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT
siSG4410	79 A G ---	---	

stSG443	65 C T ---			AGCAGATCAGTCAGCCCACTTGTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA[C] TGTATGCAATGAGAAAATAACCAACTGGTAGGATGGGGAGGGGAGGAGGAGGGAATAGGCAC AAATGGAATCTATCTGCTGCTCTCTCAGGTC
stSG4430 a	54 A G ---			ATGCACATTAAATGAATGGCCTAACTACTGGGAACCTTTAGTAGTTCTATAAGGTA/GIATTAACATA GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT CCTCCCTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCCTCCCGCCACCCAGGCTCT CGCTAGCCCTGCCCTCTGGGTCAGTGC[G]/ATGGGTTAGGCCCCCAAAAA
stSG4448	99 G A ---			ATTAGCCATTCTTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT TAACTTTGGACAACCTAAACCTTA[T]/CJTAGTGACATTGCTGTCTAATAATCAAAATACTTTCATCATA GGCTGAACATAATTATTAAGAGCAAAAGTTACCCCTCCC
stSG4449	92 T C ---			CAGACATGAGGGATGGCCCTGTCTCTCTGGGACAGAGCCTCA[C]/AJAGATGATGTCCATGTTTGTGT GAATGAAACTCAACACTCTTCAGTTTTTAGAGTCATTTTCTGGTATCGAGCGACACACCGGAGGAG CACACCCTGCTCCAAAGGCTGCTGCCCTCTGACACAGT
stSG4467	42 C A ---			ACATGTCATTTCTGACCAGG[A]/CJATTAATAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGA TTAAGAGACACAACACTGGACTTTGTTTCTTTACTGTAGCACCCAGGTTTCATG
stSG4475	21 A C ---			GTAACATTTCTGGGGTGGGGGTGAGACAAAC[A]/GJATGAACCAATAATAATTACAATTATACATT TCAAGGAGACTTTTAACTAGGTTAATGTGAACGCAGCCATCAATGTTTGTGAGGAAAGGGAGA TGAAGTCTGCTCTGGGGCAACGTTTGGCCTCATTCGAGTCAGACTGGC
stSG4477	32 A G ---			TGAACTCAGAGCTGGTGGGAGCTGCAGCGAGGGAGGCTGGGGCCAGATGAGCCGCCGGGA CAGCAGGCTCG[C]/GCCACGTCTGCGTTGTGAAGAGGACATAGGCTGCCCTGGACTCGATCT GATTCATTGACAGGGGAGACGCTGTTGTCAATCA
stSG4531	79 C T ---			TGCATTAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGTAGGAGACAGAGTCTATTT AAAAGAGACAGTGGGCACC[G]/CAATTTGGAGGGGAAGCGGGGCAGGGTTTAGAGAAC
stSG4550 b	86 G A ---			TGCATTAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGTAGGAGACAGAGTCTATTT AAAAGAGACAGTGGGCAC[C]/GCAATTTGAGGGGAAGCGGGGCAGGGTTTAGAGAAC
stSG4550 a	85 C G ---			AATCAGGCACAAGCTCGGGAGAGAGCAACAAAGCTCTTCTGCAC[A]/GJATGGGAGGGAGACAC CAATTGAAAAGGCATGTTCTTCTTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
stSG4590	47 A G ---			AACTGTATCACCCAGCGGT[G]/CJAATGTACTAGTACTGTTCCACAGGGATTTTATACTATTC CTATAAGGTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTCACATTTATCT TAATATTCCTGTTCAAGATGCTCTGGAG
stSG4623	22 T C ---			TAAAAAAAACAACCCCCCAAAAAACCCAGAGTTTGTAGTTTATGTTTTCAGATTTAAAG GTATTTCTTTCTTAGCTTCTAAATTTTGAGTCA[T]/CJATCAGAAAAGTCTTCCCTACTCCAAAGGTGA GAAAGGA
stSG4843	102 A C ---			

stSG4850 a	38 C T ---	---	GGATCTAACTGGGAATGCCGAGGAGGAAGGGCTC/TGTGCACTTGCAGGCCACGTACAGGAG AGCCAGCGTGCTGTGGGGAGGTTTCCAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGAATCTTGGGTCCC
stSG4879	86 A G ---	---	AACCTTCC AACTCTGAAGGGGTGACCTCAACCCAGCCCTTGTCTGTGAGGTCTGCTTTTGAGAATGGCCTG CCCTGGGACTGGAGCAG/A/GCTTGGGTGAGCTCTAGGTGAGGGTGGTGGAGGGGCATAGAAAT AACTTCC
stSG4885	104 G A ---	---	ACTGGACTGGCTGCTTGTGAGCCGGCTGAGCGGCTGGGACTCGGCTGACCACTCGCTCTTTCAG AGACTCGCCCGGTGACCACTACGCTCTGCC/G/AGTGGGAAAGCAGAGCAGGACC
stSG4896	112 C T ---	---	AAACAATCAAAACCAATCCAGCAGTCTATGTACAGGGCCACTCCCTGCTCTGCCATAGAGA GGTGGGGGCAGCTGAGGAGTGGTGGGGCTGGGCACTTTTCT/TCAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A ---	---	ACAGTCCGATGGTTACACAA/TG/ATTTAAATGTATTTAAATCCCACTTACGAATGATTAATGA TAAATCTTATGTTTATTTATCATCACTACCAAAAGGTGGGTGAGGGTGTGTTTCTGTCTCT
stSG4950	24 A G ---	---	TCATGACTCCAGGAAAGGTCTT/AGTCTTAGCTTCTCTCCCTACTTTCTCTACATGTCAGC ACTGTAATGTAGCTAAGATATAGGCAATGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---	---	AGATACGGGCAAAACACTGGGATGGCTTCTGACAACTTAAGAGGTCTCCGAGTTATTTCTGGTT GGGAACACTGACCCAGCCCTTATTCCTTCAAGGACTGTAGTCATTGGCAAGGAGGATTCATGAGCC CC/G/AGTACACAGATGGGGCCCTGCTCTATATTCAAC
stSG4961	91 C T ---	---	GAAGGTCTCTGAGGAGGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGTA/C/TAGAGAGGGCATTGAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---	---	ACTGGTCCCTCTCAGCAGATTCAGGGGTGTCAGGGCTGGTTACCAAACTCAGTAGGAGTGCAA GGGCT/AG/TACCCCGGAGCTAGACAGCCCTGGGTTGAATCTCAACTTCTCCCTTTTCTTGTGTGC AACCTTG
stSG4997	22 T C ---	---	CAAAGGAGTAGGAGCCCA/T/C/TJTAAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTGTATAGTTATTACACATGTTTAGAAGGGAGGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG6312	37 C T ---	---	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAACA/C/TJATGCCATCGGGGAAATAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107 G A ---	---	GCCTGGTCAAGCAAAATTCAGGACAGCAAGCAAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAATGTGATGTTTGTCCAC/G/ATAGTTCAAGGCAATTAAGAATAT GCAACCCAGAGATTTCTGTGAAAACATTTGCTCTTTGGCCTGGTGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGACAGACATG

[illegible]

[illegible]

ESTD- AT3a	--	--	--	--	AGACCTCAGTTTCTCTCTGTAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAAGGTGGAGGAATTTGAAAGGGCATTG GAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAATGTGG
ESTD- B3AR	--	--	--	---	GGCTGCCAGGGTTCCGTGGAGGCGGCCCTAGCCGGGGCCCTGCTGGCCCTGGCGGTCTGGCCACCC GTGGAGGCAACCTGCTGTGTCATCGTGGCCATCGCCCGGACTCCGAGACTCCAGACCATGACCAACGT GTTCTGACTTCCGTGGCCGACGACCTGTTGATGGGACTCTGTTGGTGGCGCGGGGCCACCTT GGCCG
ESTD- BA511	--	--	--	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGTGCCACTGCA
ESTD- BCL2	--	--	--	---	AGCTGGATTAACTCCTCTCTCTGGGGCCGTGGGGTGGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAAGGATGGCGACCGCTGGGAGAACAGGTACGACAAACCGGGAG ATAGTGATGAAGTACATCCATTATAGCTGTCCAGAGGGGCTACGAGTGGGATCGGGGAGATGTGG GGCCGCGCCCCCGGGGGCGCCCCCGCAACCGGCATCTCTCTCTCCCA
ESTD-BCR	--	--	--	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTCGGCAAGA GACCAAGAGGTGAGCTTCTGTGTCGCCGGAAGGGAGGCGAGTGACAACTACTGCTTCAAA ATCAACCATCCGTTGGACACTGTGGCTGCCATCTGCCCTGGCACA
ESTD- BRCA1a	--	--	--	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	--	--	--	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAAGTACAGTGAGGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAGCCAGCTCAAGCAATATTATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	--	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTCTGAAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTCACCCATACACATTTGGCTCAGGTTACCGAAGAGGGGGCCCAAGA AATTAGAGTCTCTAGAAAGAGAACTTATCTAGTAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTAATTTGCTCCGGGAAGCACATTCATCAA CCAGTCAAGTTGGGGGACAGCCATGACCTGAGCCCTCTGTAGCCCTTTCACACCATGATTCATCTAA GCTCTGCAAAAT

ESTD-C7						ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22						GGCAAGTTTTTATTGATAGAGGAAATCAAATAATGGCAATGAGGAGACATCACTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGTTGCTCTTCCCGGCTTCTCTCACACAC
ESTD-CB23						TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGTGCTTTCCCGGCTTCTCTCACACATACACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAAACGTGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24						ACCAGGACAGACAGCTCTCAGAGAACCCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGTGCCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCCCTGGCCACAGGCTTCTACCCGACACGTGAGCTGGTGGGTGAATGG GAAGGAGGTGCACAGTGGGGTACGACAGACCCGAGCCCTCAAGGAG
ESTD-CB25						GTTTCTTTCAGACTGTGGCTTCACTCCGGTAAGTAGTCTCTCTTTCTCTCTATCTTGGCGCTC TCTGCTCTCGAACCCAGGGCATGGAGAAATCCACGGACACAGGGCGTGAGGGCGGAGAGCCACCTG TGCACAGGTACCTACATGCTGCTGTTCTTGTCAACAGAGTCTTACCAGCAAGGGTCTGTCTGCCACC ATCCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27						TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTTGGGCTGGTTGCATTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGACCTATCTTCTGA TTTAGGGAAGCAGCATTCCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCTGCT TTCTCCTGTTTCATCCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD-COL2A1c						AGAATGTATATAGTCTCAAACCTGGCCATCTCCATTTTCAGTCCAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCTGTCAGTTTCAGGGTGTTCAGGTGGAAAAGGT GAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGTGAAGTCAACTCAAGCATATACAATACTGCCTTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1d						TGAGAGAACACCTAGTCTCCATCCTTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAAACACTGGACTTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTATGGCAAAGATATACAATAACAATTTTATTGACCAACACATATCATGGAACAGC ATT
ESTD-CPT2						GCCGCAATGCCGGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTGCTTAGAA GGCAATCCATCAAAAAGTTAACTCTGGGCAGATGAAAGCTACCATCACTTCTCATCATGAAAAC TGGAGGCGCGGCATAGTGCCTATGCCGTATCCAGCATTTTGAGAGGCTGAGGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTGGCCAACAT

ESTD- CTLA-4	--	--	--	---	---	ATGGCTGGCTGGATTTCAGGGGCACAGGCTCAGOTGAACCTGGCTACCGAGACCTGGCCCTGCAC TCTCCTGTTTTTCTCTCTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCGGAGCATGCCAGCTTTGTGTGTAGTATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGCCAGCGTGGTCGAGGTGGTACCAATCCCGGCAGAGAACAGTGTCAGCCACCACCTATGCACAGGT TCTCATCATGAAGCTGCTCAGGGTTCCCTTGGCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAAACATTTAACACCTTTTCAATCATATACACCATAAATTTCCATTTTACATAAGTCAGTT TGAGCTGAGTTTCCAAATTACTTGCAATCTAAATGTCAATACTGATTAAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTTATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAAGCTCCTCTGGGGCGGTG GGGTGTGGCTATGTGGTGTCTGTGTAGACGGGGCTTTGGTTTCAGTTGCACCTATTGCGTTATT GCAGATTGCTTTGCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCTGGCCCAACATGGGAAATACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCCTATCGTAATCCAGCTACATCGGGAGGCTGAGGCAGGAGAAATGCTTGAACCCA GGAGGCAGAGCTTGCACTGAGTGAAGCAAGATCACACCACTGCACCTACAGCCTGGGTGACACAGTGGAGA CTCTGCTCAA
ESTD- D3S11	--	--	--	---	---	AACTGATTAGAACCTGAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTAAATAAGAAATTAACAGAAATATCATTTGT TTATCAAACCTATTAACACTTATTTATTGGTAAGCCATACATAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTGTATTAAATCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAATATGGTCAGGTTACAGCTGTTATCCC AGAAGTGAACATACCTGCTCTAGAGCCAGAGTACATACTGGATGTTCTGTTTCGGTCTTACGATGG CAGGTATGAATATAATACTGTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATGTATTT CTTAACAATAAATCTGAAAGTCCAAATTTACTCCTTGATCCATGGACTGCAGAAATAATGTTATTT TAGCTGTGAGAAACAATACTAATCTTGATATGTTTCATGAGCCCTTGGGTGACCCAGGTGTAAT GCCAATAAGCAGTAATTTTGGAGGGAATCTGTTTCAATGCAGTAG
ESTD- D4S95	--	--	--	---	---	CTTTCATGCAGATAGGCTTCTCTACTAATACAGAAATTTTGAGAAGAGCAAAACAACCTTCAAGG ATAATGGGGCAATCATTCTTCTTCTTTAGAGTCTACCGG

ESTD- D7S399	--	--	--	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAATGTATAAATCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCTACATCATCTCTTTCACAAACATTTTCATCCATGGACTCCATACATAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	--	--	---	---	---	GTGGGACACCGAGGGCTCAGGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTGGCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGAGTGGGAGGAGACA GAATGCTGATTATCTGGTGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGCAGCTGCTTCCAAAGCC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD- DRD1	--	--	--	--	---	---	---	TCCCAGCCTATCGGTCAATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAG ACAAACGGTCAGCACCCAACTGAACCTGCAGATGAATCTCTGCCACACATGCTCATCCCCAAAGCT AGAGGAGATTGCTCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	--	--	---	---	---	TCTGCTTTGTGAGGAGGCTGCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTAGAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCCG TCCACCCAGGTCTCCACAGCACTCCGACAGCCCGCCCAACCCAGAGAAGATGGGCATGCCAAAG ACCACCCAAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	--	---	---	---	AAGCAGTGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGAGTGTGGCGGGCCTGGCTGG CACCTGTGGAGTCTCTGCCCCACAGGTGTAGTTAGGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGAGGTGCGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERB82	--	--	--	--	---	---	---	TCTTCAGGATCCGATCTGGCTGTGGTGGCATCGCTCCGCTAGTGTGACGGCTCCACCAGCTGG GGTAGGGGTGGTGGTCACTGTCGGGGGGGGCGGTGCAGACCCACCGGGCTGGGAGGACTTCAACC CGCCTCACTCCGTTCTCTGCAGCAGTCTCCGCATCGTACT
ESTD- ETS2	--	--	--	--	---	---	---	ACTCACAGTGTCTTTAAGTGAAATGGTGCAGAAAGAGGACACAGGAAGCCGCTCCTGGCGCCTGGCA GTCCGTGGGACGGGATGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGCTGTGGACACACAC AGACTATTTTAGATTTCTTTTGCTTTTGCAACCAAGAACAGCAATGCAAAACTCTTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCAATTCAGAAGTTAGTTG
ESTD-F2	--	--	--	--	---	---	---	GATAAGTACACTGAGGCCCCAGGAGTTATTGCCTAGTAGCCCCACTGTGCATGCACGCTTAACCTCT GCACCAATGGCCTCCAAGGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCG AGCCAGTCCCGCGGTGCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	--	---	---	---	AGATCCTGATGATTTTTCCTATTTTTCCTAAATGTTTACAGTTTGAAGTTTATGATTTATGCCCA TGCTCCATTTGAGTTAATTTGTAAAGTATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC

ESTD- G00H	--	--	--	---	---	CGCAGACCGTGCTGGGGTGGAGTGTGGAGGGAAGGAGGGAAGTGGGGGTTTAGGGACT TTCCGGGTGACTTCCCGTTCTGTCTTGCAGAGAAGGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTCGCACCGTGTGTTCTGTCTGCCCTGTTGAGCTGTCTGTGCGCGCAGTCGA CTCTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	--	--	--	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGTGTACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAATCCCCACCCACACCTGGCTGG AGCAGGAAATGCCGAGCGGCCCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAAGCTGTCCCAGGTACAG
ESTD- GNAT2	--	--	--	---	---	GACCTGAGTAGCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCACAGGCATCATG AAACCAAGTTTCCGTCAAAGACTTGAATTTCAAGTAAGTGCATGGTTCCCTAGG
ESTD- GPPK2L	--	--	--	---	---	AGTCTTCATCTGCGGTGTCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD- HPRAS	--	--	--	---	---	CTGGGCTGCGCCGACAGCTGCTGGCACCTGGACGGGCGGCCAGGCTCACTCTATATAGTGGGGTGG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	TTGAAAGTTCTCCACTGTTAACCCAGTCTATGTGGCAATGTGCCCTGGCCCCACATTTCTGGCCTTG AGGGCCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTCACCAAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTGGGCCCTCCGGCTTGATTCC AGATGGAGCTTCTTATCCCTGATGATTGGATTGGCTTCCCTGCTG
ESTD-HT2	--	--	--	---	---	GGGTAAATTTCCGAGCACTTGCATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTCAAGAGAAATAAAAGGATAACCTGGGGTTTCTGTGTC TTTGCTTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAAGCGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	ACCAACGAGCCGCGATACAGACACTCTTAAGTTTTCGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAAGTAAAGTTCTGGGTGCCCTTCTATCGCAAGAATCGTACTTATTTGAATAGTAGAGGTAA ACCACAGCCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCCCGTAGCCTAAA TGACAGCCGAAGAGGGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	AACACACAAGCCCCAGCGAGAATTGAACCTCGCGACCCCTGGTTTACAAGACCAGTGTCTAACCCT GAGCTATGGAGCCCTCGTCTGCTGTGGTTTCTTCCTTTCATCTTATAGATTGATGTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTAGCTTGAGTAAATCCAGGATATTTCTCCTACAAAATGAAA ACATTTTGTGCTCTGTAAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	--	---	---	ACCCAGTGGAGCCCGCTCATTCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGGAAGATGTTC CAGGCGACACATAGCTTAGTGGAGACTC

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ESTD- IGHV4-8	--	--	--	---	---	TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCTACATTGTGTGAGTGACGGGCGAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTGAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAAGTGAAGT ATGTAATACTTCAAAAATACTAATAACGGAGTTGAATATAAAACCCCA
ESTD-IL1A	--	--	--	---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTATTATTATTATTTTATTTTGTG AGATGGAGTCTGGCTGTGACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTATGCCATTCTCTGCCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	--	--	--	---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCTCTACCTGGGTGCTGTTCTCGCCTCAGGAGCTCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAATGCAATTTAAAGTAACCTGCTAAAGTTTTTCCATTAAACCACCTATTACTTCTAAG AGAACTGTACATGACAAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCTCACCCCTCCCTAGCCCGTGGGAAGCAGGAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCTATCTCTCCGCTCAGGTTACCACGTCACAACTTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATGTACCGTAGCAAAACTGCATTGGTATTAGA AAAAATAAAATTTCCAATATGTAGTGTGTTATACCTGCCTCTGCCATGCAGCATATAGCCTGT GGGAACAGGAGGCTTCCCTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTTCCCTTACCCATTCACTGAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTCTGCCCTGCTGCTGCTGCTGCA AGGTTTTGCTTAATCTCAATTCAATGTCTCTTTCATCTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTTAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTATAAAAATTTTTCACCTG
ESTD-MOC	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCGAGCTCTGTCCCTAGCCGAACCTTCAGGACAACGTGCAG
ESTD- METH	--	--	--	---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTTCCAAAGGTTTGGTCTAAGTGTCTAAGTACCCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCCTGTTTAGCATGG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAATACTATACCAGATCCACAGACTGATATGGCTGGT

ESTD- NFKB1	--	--	--	---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAAGAGAAA AAATTTAAGGGTGACTATTATCCACACTGCACACTGCCTAGCCCAAAACGCTCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAATCTGAG AAACTTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD- NPPA	--	--	--	---	---	TGTCCTAGGCCAGCCCTGCTTGCTCCTCGCTGTTATCTCAGTACTGCAAAAGAGAACACAGAC AT
ESTD- NFRMP	--	--	--	---	---	GGAGGAGGAGGTGGGAGGGGCTGTCTGCTCCAGGTOCCACAGACAGAGAGGCGCTCAGTGG TATCCCAACCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD- NFRAS	--	--	--	---	---	GTGTTTCTTAATCTTTTCCAGGAACACAGTGACCATAATCTTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATCTTTTGTGTTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTAACCTTGGCAATAGCATTTGC ATCCCTGTGGTTTTTAATAAAAT
ESTD-OTC	--	--	--	---	---	GTGACCTTCTCCTTAAACCTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAATTTAGGATAAACAGAAAGGAGGATGTAAACA
ESTD-PAI1	--	--	--	---	---	GCCACCAACCCACCCACAGCACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGCCCC TCAGGGCACAGAGAGTCTGGACACGTGGGAGTCAGCGGTATCATCGGAGGCGCGGGCAC ATGGCAGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCAAGTCTCTAGACAGACAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	--	---	---	CTCTTCAGGAACCACTGCTCTTACCAACACGACTTATTGCTGTCGAGAGGTACACCCGTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATCTGCCT AATCGACTGGCTTTCATAGCTCTGTGAGTGTCTTCTTCACTTTTCTGTTCTAGAACGTTTCTTAG GACTGGCAGTTTAAGCTTTCACITTAGGCTTCTGTATACCCATGCCC
ESTD- PBDA	--	--	--	---	---	CCTTCTCATGCCAGATGGAATTCAGTCCCTCAGGATCTGCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAATCTCTACCCGAGCTTGCTCGCATACAGAG GACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
ESTD-PS-1	--	--	--	---	---	GGGGAGTAAACTTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCACTAGCCTATTTCGTAGCCATATTAATTGGTTGTGCCCTTACATT ATTACTCTTGCCATTTCAAGAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTT CTACTTTGCCACAGATTATCTTGTA
ESTD- PXMP1	--	--	--	---	---	ATGAAACATGGTCTTTAATTTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGGACAAAGGTGTTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTATAATCTT
ESTD- Per/RDS	--	--	--	---	---	ACCTACAGACGTGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCGGGCTGGCTG CTGGAGAAGAGCGTCCCGGAGACTGGGAAGGCTT

ESTD-PDS	--	--	--	--	CCGAGGAATCTGAGAGCGAGAGCGAGGCTGGCTGCTGGAGAGAGCGGTCCGGAGACCTGGAAAGG CCTTCTGGAGAGTGTGAAGAGCTGGCAAGGGCAACAGGTGAAGCCGAGGGCGCAGACGAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGAACTGAGAAATAGTGCACT CCAAGAAAGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	--	CTTGACGGGAGGTACGTCCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACATTTCCC CTGCTGACAGTGTATGACAGCGAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCCG TCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACTGCGCTGGGGCCAGCCACT CCGAGTCGGCATGTCACTACGGGCGAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	--	TGAAGACCTGTGTGTCGGAGCGAGGTGTGTTCTCCTGGAGCTGAGGAGTTGTGTCTGTGTG CAGTCCCGCGCCACCTGCTGTGTTGAGCCTGGACATACACCTTCACTTCCCTTTGGCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTGTGACACACCCTGTGTGAAGACCCCAACCCCTGCCTCC CCACCCAGCCAGTTCTCTAGCAAGGCGCAGGAC
ESTD- SSA1	--	--	--	--	TTCACTTTGTGGATTGTTCTTTTGTGTGTCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCCTGTGCTGTGGGATATTTGAAGAGATCTTTCAGTCCCAATGTCTAGAGAG TTTTCCCAATGTTTCTTGTATAGTTTTCATAGTTTGGGCTTAGATTTAAGTCTTTAATCCATTTTG ATTGATTCTGTA
ESTD-TAT	--	--	--	--	AAATGTCAGGACCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTGTACAACCTTTCTTCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAATTTTAAATAGGACCCATGAGACACATCA
ESTD- THRB	--	--	--	--	TGCGGCTTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTGATTTCCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTCCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD- TNFA	--	--	--	--	TTCTGCATCTGTCTGGAAGTTAGAAGGAACAGACCACAGACCTGGTCCCAAGAAATGGAGG CAATAGGTTTGGAGGCGCATGAGGACGGGTTTCCAGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCTCACTTCCAAATCCCGGCCCCCGGATGG
ESTD-TYR	--	--	--	--	TAGTGAAGTTTTCATCTCTCTGCTGAGTCTCTGGATTCTTGTTCACCCGCAACAAGAGTCTATGC CAAGGCAGAAAGCTGGTCTCATGGGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCAATAATATTGATGTCTGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

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EST11458 6	--	--	--	---	---	CCACTTTGGTAGTGGCAGTGTGACTCATCCACAATGATTCTCCAGTGTCTATCTTGTTCTCGAGTTTT CTCTGCCATGTTGCTATTGCGAGGACCTGTCCAGCAGATGATTTACCATTTTCCACAGTGGT CCCATTAACAAACATTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGTCTCCTTCCAGGTATTGTTGCAGAAGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAGGCCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGGTGAACCTGGTCTCTTGCCATTGCGGCCCTCTCGGGGCCGTGG TCTCTGGTGTGGTAGTCTGGAGTCAAGGTGCTCTAGTGAAGCTGGTGGTGGCAACC CTGGGAACGATGGTCCCCCAGGTGCGATGGTCAACCCGACACAAGGGAGCGCGGTACCCCTGG CAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCACTTCTACAGGGCTCTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAATATCTTCCCTCTAGGATGAGGTGA TAGTAATGACCGATGGGGTCAAGAACTGTTCTGTCAACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST78807 EST44438 7	--	--	--	---	---	ATGCTAAGGGGATCGGACATGAAGGACCTGTGAGCCGATTGTCTCTATCTCCAGGGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCCCAGGCACTGGGCTCCGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCACCATGCCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCT GCTCCGACCTAAGCGGAGAGCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGAAGTATTACTGAGTAAGGGAACCTTGAATGTTATTCAACTGG ATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATAGTACTTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCAGCTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTGTGTTGTTGTTACTA TAGTCCAAAGTGAA

EST10398 2	--	--	--	---	---	---	TGCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTTATCTACTTATCTATGATGATGTTACACTTTGGGGCTTGACTTTCCAACACGGAGAAG CATTGTTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGCTATTAGGCATTGG
EST36751 7	--	--	--	---	---	---	CCAAGTCGTTCAATTTAGCTTTCAGGTTTTAACTCGATTACTTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	--	--	--	---	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTTCACTGGATGCAATTAATAACAAATATTTACCTTTTGAATAAATAATG AAGGATTTGACCTGCTTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTTTGAACAATACAGAT GCCTCCCTGTAGCAGTTTTACGCCCTCTCTACCCCTA
EST18288 3	--	--	--	---	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCAAGAACTGGATGTTGCTGAGAA GATTGACAGGTTTCATGACAGGCTGTGACAGGATGGAAGACTGGCTGCTGCTGACGGGAGCCAGTGTGG ACAGACCCCTGGCTTTCAACACCTACGTCCACTTCAAGGTAAGGCAAACTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	--	---	---	---	TTCCGGCAGCCCCCATCTTGGACCTGGTCCCTCAGGGGCCACCCCGGGCACTCACCGCTCT CGCTCTCGGTAAACATCCGGCGGGCGCGTCTTGACACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGCTTGGCAGGGCCAGCCCTGACAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTTG
EST58707 7	--	--	--	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATACCTTAATCATTTGTTACAGGAGGCTTT AAGTTACGATCTTTGGCTACATGAAGGCCAAATTCGAGAGACCTAGAAGATACACGAGACCGA ATGTATCAAAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTCTGGTAGGCCAGGTTTAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	--	--	--	---	---	---	AGACCATGAAGGAGTTGAAGGCCTACAAATCGAACTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGCTGTCCAAGGAGCTGCAGGGCGCAGGCCCGGCTGGCGCGGACATGGAGGA CGTGGCGGGCGCTGTGTCAGTACCGGGGAGGTGCAGGCCATCTCGGCCAGAGCAACCGAGGAGC TGCGGGTGGCTCGCTCCACCTGGCAAGCTGGTAAGCGGCTCTC
EST43211 8	--	--	--	---	---	---	CGCTGTTGTCAGTACCGGGGAGGTGCAGGCCATCTCGGCCAGAGCACCGAGGAGCTGCGGGTGG CCTCGCTCCCACTGGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAGCGGCC TGGCAGTGTACAGCGGGGGGGGGAGGGGCGGAGGCGGCTCAGCGCCATCCGCGAGGCGCTG GGGCGCTGTGTGAACAGGGCGGTGGGGGGCGGCGGCTGTGGGCTC
EST36770 4	--	--	--	---	---	---	TGTAGCCAAAGTCACTGCATCATCTTTGGCTGCTGGCAGGCTTGCCAGCTTATGCACTATATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAAATATACTGGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTATACCTTATTGGAAGGCCCTAAAGAAGGCTTATG

EST26021 1						TAATGTAAGCTCATCCACCAGAGCCTGCACCATGTTTGAGGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTGTGAAAGAGGAGCAAGAGAACATTCCTCTGCAGCAGCTTCACCTACCAAAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTCTTTTGCACAAGACAAAGCAAGGCC
EST51212 0						ATCCTGAGCTCGCAATAAGCTTCTTGGTTCTACTTCTCTCCACAAGCCCCCAATTTACATTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTCTCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2						GTTCGAAATCTCTCTGAAAGTGGCCGGTTTAACTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGCCCTTGAAGCTGGAGTGGGTTTAGGACGGGGTCTCTGCGTGCATCTTAAGCTCT GAGAGCAAACTCCCTTGAAGCTGGGAGTGGGTTTAGGACGGGCTCTCTGCGTGCATCTTAAGCT CTGAGA
EST53018 6						ACAATCCAGGTCACACATTCAGAAAGAGGGGTGTCAGTGAGCCTGGGTAGGTCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5						CTTCTATGGGATTGACTTTATTTTCTCATTGCTTACCCTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGACGTCATGACAAATTTGAAGCTGACAAATTACACAAGAGGAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTGAACCTGGTGTACCTTTAATTACAACTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
EST34088 2						GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCACAAGAGACCGGCTCAAGG ATCCAAAGGCCCACTCCCGAACCCTCAGGGTCTCTGTGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5						CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCCCTTGGA CTTTGAGTCAATTTGGCTGGACTTGAGTCCCTGAACAGCAAGAGAAAGAGACCCCGAGAAAT CACAGTGGGCACGTGCGTCTACGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082 0						TCAGGGTGGCTGGACCCAGGCCCCAGCTCTGCAGAGGAGGACGTGGCTGGGCTCGTGAAGCATG TGGGGTGAGCCAGGGGCCCAAGGAGGACACCTGGCTTACGCTGCTCAGCCCTGCTGTGCAC CCAGATCACTGTCTCTGOCATGGCCCTGTGGATGCGCTCTGCCCCCTGCTGGCGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGGG
EST45311 0						GGCCTCCTCTCTCCAAATTTGTCCCTATAGTTTCCCTATTAAAGTGAACATACATTCATTTTAGT GGATAGATGCACACAACACAAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAATCACCTCTTTCATTTAACAGCCCTATTCAATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTGTGTAAT

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining
comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12Q 1/68, C12N 15/11	A3	(11) International Publication Number: WO 98/20165 (43) International Publication Date: 14 May 1998 (14.05.98)
(21) International Application Number: PCT/US97/20313 (22) International Filing Date: 5 November 1997 (05.11.97) (30) Priority Data: 60/030,455 6 November 1996 (06.11.96) US (71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Massachusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA). (74) Agents: GRANAHAH, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).		(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 12 November 1998 (12.11.98)
(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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INTERNATIONAL SEARCH REPORT

International Application No.

PL 1/US 97/20313

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12Q1/68 C12N15/11

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 12607 A (MOLECULAR TOOL INC) 11 May 1995 see the whole document	1-20
X	WANG D ET AL: "TOWARD A THIRD GENERATION GENETIC MAP OF THE HUMAN GENOME BASED ON BI-ALLELIC POLYMORPHISMS" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 59, no. 4, October 1996, page A03 XP002050641 see abstract	1-20

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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
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- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

B document member of the same patent family

Date of the actual completion of the international search

17 June 1998

Date of mailing of the international search report

23.09.1998

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INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 97/20313

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL10 embl Accession number: hst27766, 12 January 1995 ADAMS M D ET AL.: "Initial assessment of human gene diversity and expression patterns based upon 52 million basepairs of cDNA sequence" XP002067789 * Sequence *</p>	1-3,10, 11
X	<p>SYVANEN A -CH ET AL: "IDENTIFICATION OF INDIVIDUALS BY ANALYSIS OF BIALLELIC DNA MARKERS, USING PCR AND SOLID-PHASE MINISEQUENCING" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 52, no. 1, January 1993, pages 46-59, XP002050638 see abstract see page 47, column 1, paragraph 3 - page 50, column 1, paragraph 1 see page 51, column 1, paragraph 3; figure 1; table 1</p>	1-3, 7-10,13, 14,17-20
X	<p>FR 2 722 295 A (ROUSSY INST GUSTAVE) 12 January 1996 see abstract see page 1, line 5 - page 2, line 17 see page 9, line 9 - page 10, line 15; tables 2,3</p>	1-3,7-9, 17-20
X	<p>HRUBAN R H ET AL: "K-RAS ONCOGENE ACTIVATION IN ADENOCARCINOMA OF THE HUMAN PANCREAS A STUDY OF 82 CARCINOMAS USING A COMBINATION OF MUTANT-ENRICHED POLYMERASE CHAIN REACTION ANALYSIS AND ALLELE-SPECIFIC OLIGONUCLEOTIDE HYBRIDIZATION" AMERICAN JOURNAL OF PATHOLOGY, vol. 143, no. 2, 1 August 1993, pages 545-554, XP000572114 see the whole document</p>	10-16, 18-20
X	<p>GROMPE M: "THE RAPID DETECTION OF UNKNOWN MUTATIONS IN NUCLEIC ACIDS" NATURE GENETICS, vol. 5, no. 2, October 1993, pages 111-117, XP000615290 see the whole document</p>	18-20

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INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 97/20313

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>NIKIFOROV T T ET AL: "GENETIC BIT ANALYSIS: A SOLID PHASE METHOD FOR TYPING SINGLE NUCLEOTIDE POLYMORPHISMS" NUCLEIC ACIDS RESEARCH, vol. 22, no. 20, October 1994, pages 4167-4175, XP002015765 see the whole document -----</p>	18-20

INTERNATIONAL SEARCH REPORT

L national application No.
PCT/US 97/20313

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-20 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-20 (partially)

INVENTION 1: An isolated nucleic acid segment including a polymorphic site having the nucleotide sequence of SEQ ID NO:1149, or the complement of that segment or portions thereof, an allele-specific oligonucleotide probe or primer hybridizing to such a segment or its complement, and a method of analyzing such a nucleic acid by determining the bases occupying the polymorphic site(s).

2. Claims: 1-20 (partially)

INVENTION 2 to INVENTION 2669:

-Idem as invention 1 but limited to the sequences having SEQ ID Nos. 1150 to 3817. (Invention 2 is limited to SEQ ID NO:1150, invention 3 is limited to SEQ ID NO:1151, ..., invention 2269 is limited to SEQ ID NO:3817).

For the sake of conciseness, the first group is explicitly defined, the other groups are defined by analogy hereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PC/US 97/20313

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9512607 A	11-05-95	AU 8132194 A	23-05-95
		CA 2175695 A	11-05-95
		EP 0726905 A	21-08-96
		US 5762876 A	09-06-98

FR 2722295 A	12-01-96	NONE	
